

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald

(ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS

(iii) NUMBER OF SEQUENCES: 355

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 05-MAY-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.411C9

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

205220" CH8800T

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGCACCG	GTAGTTTGAA	CCAAACGCAC	AATCGACGGG	CAAACGAACG	GAAGAACACA	60
ACCATGAAGA	TGGTGAAATC	GATCGCCGCA	GGTCTGACCG	CCGCGGCTGC	AATCGGCGCC	120
GCTGCGGCCG	GTGTGACTTC	GATCATGGCT	GGCGGCCCGG	TCGTATACCA	GATGCAGCCG	180
GTCGTCTTCG	GCGCGCCACT	GCCGTTGGAC	CCGGCATCCG	CCCCTGACGT	CCCGACCGCC	240
GCCCAGTTGA	CCAGCCTGCT	CAACAGCCTC	GCCGATCCCA	ACGTGTCGTT	TGCGAACAAG	300
GGCAGTCTGG	TCGAGGGCGG	CATCGGGGGC	ACCGAGGCGC	GCATCGCCGA	CCACAAGCTG	360
AAGAAGGCCG	CCGAGCACGG	GGATCTGCCG	CTGTCTGTTCA	GCGTGACGAA	CATCCAGCCG	420
GCGGCCGCCG	GTTCCGGCCAC	CGCCGACGTT	TCCGTCTCGG	GTCCGAAGCT	CTCGTCGCCG	480
GTCACGCAGA	ACGTCACGTT	CGTGAATCAA	GGCGGCTGGA	TGCTGTCACG	CGCATCGGCG	540
ATGGAGTTGC	TGCAGGCCGC	AGGGNAACTG	ATTGGCGGGC	CGGNTTCAGC	CCGCTGTTCA	600
GCTACGCCGC	CCGCCTGGTG	ACGCGTCCAT	GTCGAACACT	CGCGCGTGTA	GCACGGTGCG	660
GTNTGCGCAG	GGNCGCACGC	ACCGCCCGGT	GCAAGCCGTC	CTCGAGATAG	GTGGTGNCTC	720
GNCACCAGNG	ANCACCCCN	NNTCGNCNNT	TCTCGNTGNT	GNATGA		766

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCACC	ATCACCATCA	CGATGAAGTC	ACGGTAGAGA	CGACCTCCGT	CTTCCGCGCA	60
GACTTCCTCA	GCGAGCTGGA	CGCTCCTGCG	CAAGCGGGTA	CGGAGAGCGC	GGTCTCCGGG	120
GTGGAAGGGC	TCCC GCCGGG	CTCGGCGTTG	CTGGTAGTCA	AACGAGGCC	CAACGCCGGG	180
TCCCGGTTCC	TACTCGACCA	AGCCATCACG	TCGGCTGGTC	GGCATCCCGA	CAGCGACATA	240
TTTCTCGACG	ACGTGACCGT	GAGCCGTCGC	CATGCTGAAT	TCCGGTTGGA	AAACAACGAA	300
TTCAATGTCG	TCGATGTCGG	GAGTCTCAAC	GGCACCTACG	TCAACCGCGA	GCCCGTGGAT	360
TCGGCGGTGC	TGGCGAACGG	CGACGAGGTC	CAGATCGGCA	AGCTCCGGTT	GGTGTCTTGG	420
ACCGGACCCA	AGCAAGGCGA	GGATGACGGG	AGTACCGGGG	GCCCGTGAGC	GCACCCGATA	480
GCCCCGCGCT	GGCCGGGATG	TCGATCGGGG	CGGTCTCCG	ACCTGCTACG	ACCGGATTTT	540
CCCTGATGTC	CACCATCTCC	AAGATTTCGAT	TCTTGGGAGG	CTTGAGGGTC	NGGGTGACCC	600
CCCCGCGGGC	CTCATTCTNGG	GGTNTCGGCN	GGTTTCACCC	CNTACCNACT	GCCNCCCGGN	660
TTGCNAATTC	NTTCTTCNCT	GCCCNAAAG	GGACNNTAN	CTTGCCGCTN	GAAANGGTNA	720
TCCNGGGCCC	NTCCTNGAAN	CCCNNTCCCC	CT			752

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC	ACCATCACCA	TCACACTTCT	AACCGCCCAG	CGCGTCGGGG	GCGTCGAGCA	60
CCACGCGACA	CCGGGCCCCG	TCGATCTGCT	AGCTTGAGTC	TGGTCAGGCA	TCGTCGTCAG	120
CAGCGCGATG	CCCTATGTTT	GTCGTCGACT	CAGATATCGC	GGCAATCCAA	TCTCCCGCCT	180

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GCGGCCGGCG	GTGCTGCAAA	CTACTCCCGG	AGGAATTTTCG	ACGTGCGCAT	CAAGATCTTC	240
ATGCTGGTCA	CGGCTGTCGT	TTTGCTCTGT	TGTTCCGGGTG	TGGCCACGGC	CGCGCCCAAG	300
ACCTACTGCG	AGGAGTTGAA	AGGCACCGAT	ACCGGCCAGG	CGTGCCAGAT	TCAAATGTCC	360
GACCCGGCCT	ACAACATCAA	CATCAGCCTG	CCCAGTTACT	ACCCCGACCA	GAAGTCGCTG	420
GAAAATTACA	TCGCCCAGAC	GCGCGACAAG	TTCCTCAGCG	CGGCCACATC	GTCCACTCCA	480
CGCGAAGCCC	CCTACGAATT	GAATATCACC	TCGGCCACAT	ACCAGTCCGC	GATACCGCCG	540
CGTGGTACGC	AGGCCGTGGT	GCTCAMGGTC	TACCACAACG	CCGGCGGGCAC	GCACCCAACG	600
ACCACGTACA	AGGCCTTCGA	TTGGGACCAG	GCCTATCGCA	AGCCAATCAC	CTATGACACG	660
CTGTGGCAGG	CTGACACCGA	TCCGCTGCCA	GTCGTCTTCC	CCATTGTTGC	AAGGTGAACT	720
GAGCAACGCA	GACCGGGACA	ACWGGTATCG	ATAGCCGCCN	AATGCCGGCT	TGGAACCCNG	780
TGAAATTATC	ACAACCTTCGC	AGTCACNAAA	NAA			813

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC	ACGGCCGCGT	CCGATAACTT	CCAGCTGTCC	CAGGGTGGGC	AGGGATTTCGC	60
CATTCGGATC	GGGCAGGCGA	TGGCGATCGC	GGGCCAGATC	CGATCGGGTG	GGGGGTCACC	120
CACCGTTTCAT	ATCGGGCCTA	CCGCCCTTCT	CGGCTTGGGT	GTTGTCGACA	ACAACGGCAA	180
CGGCGCACGA	GTCCAACGCG	TGGTCGGGAG	CGTCCGGCG	GCAAGTCTCG	GCATCTCCAC	240
CGGCGACGTG	ATCACC GCGG	TCGACGGCGC	TCCGATCAAC	TCGGCCACCG	CGATGGCGGA	300
CGCGCTTAAC	GGGCATCATC	CCGGTGACGT	CATCTCGGTG	AACTGGCAAA	CCAAGTCGGG	360
CGGCACGCGT	ACAGGGAACG	TGACATTGGC	CGAGGGACCC	CCGGCCTGAT	TTCGTCCGYGG	420
ATACCACCCG	CCGGCCGGCC	AATTGGA				447

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCACTGC	GGTCGCCGAG	TATGTCGCCC	AGCAAATGTC	TGGCAGCCGC	CCAACGGAAT	60
CCGGTGATCC	GACGTCGCAG	GTTGTCGAAC	CCGCCGCCGC	GGAAGTATCG	GTCCATGCCT	120
AGCCCGGCGA	CGGCGAGCGC	CGGAATGGCG	CGAGTGAGGA	GGCGGGCAAT	TTGGCGGGGC	180
CCGGCGACGG	NGAGCGCCGG	AATGGCGCGA	GTGAGGAGGT	GGNCAGTCAT	CCCCAGNGTG	240
ATCCAATCAA	CCTGNATTCG	GNCTGNNGGN	CCATTTGACA	ATCGAGGTAG	TGAGCGCAAA	300
TGAATGATGG	AAAACGGGNG	GNGACGTCCG	NTGTTCTGGT	GGTGNTAGGT	GNCTGNCTGG	360
NGTNGNGGNT	ATCAGGATGT	TCTTCGNCGA	AANCTGATGN	CGAGGAACAG	GGTGTNCCCCG	420
NNANNCCNAN	GGNGTCCNAN	CCCNNTTCC	TCGNCGANAT	CANANAGNCG	NTTGATGNGA	480
NAAAAGGGTG	GANCAGNNN	AANTNGNGGN	CCNAANAANC	NNNANNGNNG	NNAGNTNGNT	540
NNNTNTTNNC	ANNNNNNTG	NNGNNGNNCN	NNNCAANCNN	NTNNNNGNAA	NNGGNTTNTT	600
NAAT						604

(2) INFORMATION FOR SEQ ID NO:6:

10084843.022502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCANGTCG	AACCACCTCA	CTAAAGGGAA	CAAAAGCTNG	AGCTCCACCG	CGGTGGCGGC	60
CGCTCTAGAA	CTAGTGKATM	YYYCKGGCTG	CAGSAATYCG	GYACGAGCAT	TAGGACAGTC	120
TAACGGTCCT	GTTACGGTGA	TCGAATGACC	GACGACATCC	TGCTGATCGA	CACCGACGAA	180
CGGGTGCGAA	CCCTCACCTT	CAACCGGCCG	CAGTCCCGYA	ACGCGCTCTC	GGCGGCGCTA	240
CGGGATCGGT	TTTTCGCGGY	GTTGGYCGAC	GCCGAGGYCG	ACGACGACAT	CGACGTCGTC	300
ATCCTCACCG	GYGCCGATCC	GGTGTCTGTC	GCCGGACTGG	ACCTCAAGGT	AGCTGGCCCG	360
GCAGACCGCG	CTGCCGGACA	TCTACCGCG	GTGGGCGGCC	ATGACCAAGC	CGGTGATCGG	420
CGCGATCAAC	GGCGCCGGGG	TGAGCGGGGG	GCTCGAATCT	GCGCTGTACT	GCGACATCCT	480
GATCGCCTCC	GAGCACGCCC	GCTTCGNCGA	CACCCACGCC	CGGGTGGGGC	TGCTGCCAC	540
CTGGGGACTC	AGTGTGTGCT	TGCCGCAAAA	GGTCGGCATC	GGNCTGGGCC	GGTGGATGAG	600
CCTGACCGGC	GACTACCTGT	CCGTGACCGA	CGC			633

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGACGAC	GGCGCCGGAG	AGCGGGCGCG	AACGGCGATC	GACGCGGCCC	TGGCCAGAGT	60
CGGCACCACC	CAGGAGGGAG	TCGAATCATG	AAATTTGTCA	ACCATATTGA	GCCCGTCGCG	120
CCCCGCCGAG	CCGGCGGCGC	GGTCGCCGAG	GTCTATGCCG	AGGCCCCGCC	CGAGTTCGGC	180
CGGCTGCCCC	AGCCGCTCGC	CATGCTGTCC	CCGGACGAGG	GACTGCTCAC	CGCCGGCTGG	240
GCGACGTTGC	GCGAGACACT	GCTGGTGGGC	CAGGTGCCGC	GTGGCCGCAA	GGAAGCCGTC	300
GCCGCCGCCG	TCGCGGCCAG	CCTGCGCTGC	CCCTGGTGCG	TCGACGCACA	CACCACCATG	360
CTGTACGCGG	CAGGCCAAAC	CGACACCGCC	GCGGCGATCT	TGGCCGGCAC	AGCACCTGCC	420
GCCGGTGACC	CGAACGCGCC	GTATGTGGCG	TGGGCGGCAG	GAACCGGGAC	ACCGGCGGGA	480
CCGCCGGCAC	CGTTCGGCCC	GGATGTCGCC	GCCGAATACC	TGGGCACCGC	GGTGCAATTC	540
CACTTCATCG	CACGCCTGGT	CCTGGTGCTG	CTGGACGAAA	CCTTCCTGCC	GGGGGGCCCG	600
CGCGCCCAAC	AGCTCATGCG	CCGCGCCGGT	GGACTGGTGT	TCGCCCCGAA	GGTGCGCGCG	660
GAGCATCGGC	CGGGCCGCTC	CACCCGCCGG	CTCGAGCCGC	GAACGCTGCC	CGACGATCTG	720
GCATGGGCAA	CACCGTCCGA	GCCCATAGCA	ACCGCGTTCG	CCGCGCTCAG	CCACCACCTG	780
GACACCGCGC	CGCACCTGCC	GCCACCGACT	CGTCAGGTGG	TCAGGCGGGT	CGTGGGGTGG	840
TGGCACGGCG	AGCCAATGCC	GATGAGCAGT	CGCTGGACGA	ACGAGCACAC	CGCCGAGCTG	900
CCCCCGGACC	TGCACGCGCC	CACCCGTCTT	GCCCTGCTGA	CCGGCCTGGC	CCCGCATCAG	960
GTGACCGACG	ACGACGTCGC	CGCGGCCCGA	TCCCTGCTCG	ACACCGATGC	GGCGCTGGTT	1020
GGCGCCCTGG	CCTGGGCGCG	CTTCACCGCC	GCGCGGCGCA	TCGGCACCTG	GATCGGCGCC	1080
GCCGCCGAGG	GCCAGGTGTC	GCGGCAAAAC	CCGACTGGGT	GAGTGTGCGC	GCCCTGTCCG	1140
TAGGGTGTCA	TCGCTGGCCC	GAGGGATCTC	GCGGCGGCGA	ACGGAGGTGG	CGACACAGGT	1200
GGAAGCTGCG	CCCACTGGCT	TGCGCCCCAA	CGCGTCTGTG	GGCGTTCGGT	TGGCCGCACT	1260
GGCCGATCAG	GTCGGCGCCG	GCCCTTGGCC	GAAGGTCCAG	CTCAACGTGC	CGTCACCGAA	1320
GGACCGGACG	GTCACCGGGG	GTCACCCTGC	GCGCCCAAGG	AA		1362

(2) INFORMATION FOR SEQ ID NO:8:

205220" E484800T

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGACGACCC	CGATATGCCG	GGCACCCTAG	CGAAAGCCGT	CGCCGACGCA	CTCGGGCGCG	60
GTATCGCTCC	CGTTGAGGAC	ATTGAGGACT	GCGTGGAGGC	CCGGCTGGGG	GAAGCCGGTC	120
TGGATGACGT	GGCCCGTGTT	TACATCATCT	ACCGGCAGCG	GCGCGCCGAG	CTGCGGACCG	180
CTAAGGCCTT	GCTCGGCGTG	CGGGACGAGT	TAAAGCTGAG	CTTGGCGGCC	GTGACGGTAC	240
TGCGCGAGCG	CTATCTGCTG	CACGACGAGC	AGGGCCGGCC	GGCCGAGTCG	ACCGGCGAGC	300
TGATGGACCG	ATCGGCGCGC	TGTGTCGCGG	CGGCCGAGGA	CCAGTATGAG	CCGGGCTCGT	360
CGAGGCGGGT	GGCCGAGCGG	TTGGGACGCG	TATTACGCAA	CCTGGAATTC	CTGCCGAATT	420
CGCCACGTT	GATGAACTCT	GGCACCAGAC	TGGGACTGCT	CGCCGGCTGT	TTTGTTCCTG	480
CGATTGAGGA	TTGCTGCAAA	TCGATCTTTG	CGACGCTGGG	ACAGGCCGCC	GAGCTGCAGC	540
GGGCTGGAGG	CGGCACCGGA	TATGCGTTCA	GCCACCTGCG	ACCCGCCGGG	GATCGGGTGG	600
CCTCCACGGG	CGGCACGGCC	AGCGGACCGG	TGTCGTTTCT	ACGGCTGTAT	GACAGTGCCG	660
CGGGTGTGGT	CTCCATGGGC	GGTCGCCGGC	GTGGCGCCTG	TATGGCTGTG	CTTGATGTGT	720
CGCACCCGGA	TATCTGTGAT	TTGCTCACC	CCAAGGCCGA	ATCCCCCAGC	GAGCTCCCGC	780
ATTTCAACCT	ATCGGTGCGT	GTGACCGACG	CGTTCCTGCG	GGCCGTGCAA	CGCAACGGCC	840
TACACCGGCT	GGTCAATCCG	CGAACCAGCA	AGATCGTCGC	GCGGATGCCC	GCCGCCGAGC	900
TGTTGACGCG	CATCTGCAAA	GCCGCGCAGC	CCGGTGGCGA	TCCCGGGCTG	GTGTTTCTCG	960
ACACGATCAA	TAGGGCAAAC	CCGGTGCCGG	GGAGAGGCCG	CATCGAGGCG	ACCAACCCGT	1020
GCGGGGAGGT	CCCACTGCTG	CCTTACGAGT	CATGTAATCT	CGGCTCGATC	AACCTCGCCC	1080
GGATGCTCGC	CGACGGTCGC	GTGACTGGG	ACCGGCTCGA	GGAGGTCGCC	GGTGTGGCGG	1140
TGCGGTTTCT	TGATGACGTC	ATCGATGTCA	GCCCTATACC	CTTCCCCGAA	CTGGGTGAGG	1200
CGGCCCCGCG	CACCCGCAAG	ATCGGGCTGG	GAGTCATGGG	TTTGGCGGAA	CTGCTTGCCG	1260
CACTGGGTAT	TCCGTACGAC	AGTGAAGAAG	CCGTGCGGTT	AGCCACCCGG	CTCATGCGTC	1320
GCATACAGCA	GGCGGCGCAC	ACGGCATCGC	GGAGGCTGGC	CGAAGAGCGG	GGCGCATTCC	1380
CGGCGTTTAC	CGATAGCCGG	TTGCGCGGTT	CGGGCCCGAG	GCGCAACGCA	CAGGTCACCT	1440
CCGTCGCTCC	GACGGGCA					1458

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTAAT	CGTGCTGGAT	CTGGAACCGC	GTGGCCCGCT	ACCTACCGAG	ATCTACTGGC	60
GGCGCAGGGG	GCTGGCCCTG	GGCATCGCGG	TCGTCGTAAGT	CGGGATCGCG	GTGGCCATCG	120
TCATCGCCTT	CGTCGACAGC	AGCGCCGGTG	CCAAACCGGT	CAGCGCCGAC	AAGCCGGCCT	180
CCGCCCAGAG	CCATCCGGGC	TCGCCGCGAC	CCCAAGCACC	CCAGCCGGCC	GGGCAAACCG	240
AAGGTAACGC	CGCCGCGGCC	CCGCCGAGG	GCCAAAACCC	CGAGACACCC	ACGCCACCG	300
CCGCGGTGCA	GCCGCCGCCG	GTGCTCAAGG	AAGGGGACGA	TTGCCCCGAT	TCGACGCTGG	360
CCGTCAAAGG	TTTGACCAAC	GCGCCGAGT	ACTACGTCGG	CGACCAGCCG	AAGTTCACCA	420
TGGTGGTCAC	CAACATCGGC	CTGGTGTCTT	GTAAACGCGA	CGTTGGGGCC	GCGGTGTTGG	480
CCGCCTACGT	TTACTCGCTG	GACAACAAGC	GGTTGTGGTC	CAACCTGGAC	TGCGCGCCCT	540
CGAATGAGAC	GCTGGTCAAG	ACGTTTTCCT	CCGGTGAGCA	GGTAACGACC	GCGGTGACCT	600

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GGACCGGGAT	GGGATCGGCG	CCGCGCTGCC	CATTGCCGCG	GCCGGCGATC	GGGCCGGGCA	660
CCTACAATCT	CGTGGTACAA	CTGGGCAATC	TGCGCTCGCT	GCCGGTTCCG	TTCATCCTGA	720
ATCAGCCGCC	GCCGCCGCCC	GGGCCGGTAC	CCGCTCCGGG	TCCAGCGCAG	GCGCCTCCGC	780
CGGAGTCTCC	CGCGCAAGGC	GGATAATTAT	TGATCGCTGA	TGGTCGATTC	CGCCAGCTGT	840
GACAACCCCT	CGCCTCGTGC	CG				862

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA	CCGGCAAGGC	GTCACATGCC	TCCCTGGGTG	TGCAGGTGAC	CAATGACAAA	60
GACACCCCGG	GCGCCAAGAT	CGTCGAAGTA	GTGGCCGGTG	GTGCTGCCGC	GAACGCTGGA	120
GTGCCGAAGG	GCGTCGTTGT	CACCAAGGTC	GACGACCGCC	CGATCAACAG	CGCGGACGCG	180
TTGGTTGCCG	CCGTGCGGTC	CAAAGCGCCG	GGCGCCACGG	TGGCGCTAAC	CTTTCAGGAT	240
CCCTCGGGCG	GTAGCCGCAC	AGTGCAAGTC	ACCCTCGGCA	AGGCGGAGCA	GTGATGAAGG	300
TCGCCGCGCA	GTGTTCAAAG	CTCGGATATA	CGGTGGCACC	CATGGAACAG	CGTGC GGAGT	360
TGGTGGTTGG	CCGGGCACTT	GTCGTCGTCG	TTGACGATCG	CACGGCGCAC	GGCGATGAAG	420
ACCACAGCGG	GCCGCTTGTC	ACCGAGCTGC	TCACCGAGGC	CGGGTTTGTT	GTCGACGGCG	480
TGGTGGCGGT	GTCGGCCGAC	GAGGTCGAGA	TCCGAAATGC	GCTGAACACA	GCGGTGATCG	540
GCGGGGTGGA	CCTGGTGGTG	TCGGTCGGCG	GGACCGNGT	GACGNCTCGC	GATGTCACCC	600
CGGAAGCCAC	CCNGACATT	CT				622

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGCAGCGG	TAAGCCTGTT	GGCCGCCGGC	ACACTGGTGT	TGACAGCATG	CGGCGGTGGC	60
ACCAACAGCT	CGTCGTCAGG	CGCAGGCGGA	ACGTCTGGGT	CGGTGCACTG	CGGCGGCAAG	120
AAGGAGCTCC	ACTCCAGCGG	CTCGACCGCA	CAAGAAAATG	CCATGGAGCA	GTTCGTCTAT	180
GCCTACGTGC	GATCGTGCCC	GGGCTACACG	TTGGACTACA	ACGCCAACGG	GTCCGGTGCC	240
GGGGTGACCC	AGTTTCTCAA	CAACGAAACC	GATTTGCGCG	GCTCGGATGT	CCCGTTGAAT	300
CCGTGACCCG	GTCAACCTGA	CCGGTCGGCG	GAGCGGTGCG	GTTCCCCGGC	ATGGGACCTG	360
CCGACGGTGT	TCGGCCCGAT	CGCGATCACC	TACAATATCA	AGGGCGTGAG	CACGCTGAAT	420
CTTGACGGAC	CCACTACCGC	CAAGATTTTC	AACGGCACCA	TCACCGTGTG	GAATGATCCA	480
CAGATCCAAG	CCCTCAACTC	CGGCACCGAC	CTGCCGCCAA	CACCGATTAG	CGTTATCTTC	540
CGCAGCGACA	AGTCCGGTAC	GTCGGACAAC	TTCCAGAAAT	ACCTCGACGG	TGTATCCAAC	600
GGGGCGTGGG	GCAAAGGCGC	CAGCGAAACG	TTCAGCGGGG	GCGTCGGCGT	CGGCGCCAGC	660
GGGAACAACG	GAACGTCGGC	CCTACTGCAG	ACGACCGACG	GGTCGATCAC	CTACAACGAG	720
TGGTCGTTTG	CGGTGGGTAA	GCAGTTGAAC	ATGGCCCAGA	TCATCACGTC	GGCGGGTCCG	780
GATCCAGTGG	CGATCACCAC	CGAGTCGGTC	GGTAAGACAA	TCGCCGGGGC	CAAGATCATG	840
GGACAAGGCA	ACGACCTGGT	ATTGGACACG	TCGTCTGTCT	ACAGACCCAC	CCAGCCTGGC	900
TCTTACCCGA	TCGTGCTGGC	GACCTATGAG	ATCGTCTGCT	CGAAATACCC	GGATGCGACG	960
ACCGGTACTG	CGGTAAGGGC	GTTTATGCAA	GCCGCGATTG	GTCCAGGCCA	AGAAGGCCTG	1020

GACCAATACG	GCTCCATTCC	GTTGCCCAAA	TCGTTCCAAG	CAAAATTGGC	GGCCGCGGTG	1080
AATGCTATTT	CTTGACCTAG	TGAAGGGAAT	TCGACGGTGA	GCGATGCCGT	TCCGCAGGTA	1140
GGGTCGCAAT	TTGGGCCGTA	TCAGCTATTG	CGGCTGCTGG	GCCGAGGCGG	GATGGGCGAG	1200

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAAGCAGCT	GCAGGTCGTG	CTGTTTCGACG	AACTGGGCAT	GCCGAAGACC	AAACGCACCA	60
AGACCGGGCTA	GAGGAAGGAT	GCCGACGCGC	TGCAGTCGTT	GTTCGACAAG	ACCGGGGCATC	120
CGTTTCTGCA	ACATCTGCTC	GCCCACCGCG	ACGTCACCCG	GCTCAAGGTC	ACCGTCGACG	180
GGTTGCTCCA	AGCGGTGGCC	GCCGACGGCC	GCATCCACAC	CACGTTCAAC	CAGACGATCG	240
CCGCGACCGG	CCGGCTCTCC	TCGACCGAAC	CCAACCTGCA	GAACATCCCG	ATCCGCACCG	300
ACGCGGGCCG	GCGGATCCGG	GACGCGTTCC	TGGTCGGGGA	CGGTTACGCC	GAGTTGATGA	360
CGGCCGACTA	CAGCCAGATC	GAGATGCGGA	TCATGGGGCA	CCTGTCCGGG	GACGAGGGCC	420
TCATCGAGGC	GTTCAACACC	GGGGAGGACC	TGTATTTCGTT	CGTCGCGTCC	CGGGTGTTCG	480
GTGTGCCCCAT	CGACGAGGTC	ACCGGCGAGT	TGCGGCGCCG	GGTCAAGGCG	ATGTCTTACG	540
GGCTGGTTTA	CGGGTTGAGC	GCCTACGGCC	TGTCGCAGCA	GTGAAAATC	TCCACCGAGG	600
AAGCCAACGA	GCAGATGGAC	GCGTATTTTCG	CCCATTTCGG	CGGGGTGCGC	GACTACCTGC	660
GCGCCGTAGT	CGAGCGGGCC	CGCAAGGACG	GCTACACCTC	GACGGTGCTG	GGCCGTTCGCC	720
GCTACCTGCC	CGAGCTGGAC	AGCAGCAACC	GTCAAGTGCG	GGAGGCCGCC	GAGCGGGCGG	780
CGCTGAACGC	GCCGATCCAG	GGCAGCGCGG	CCGACATCAT	CAAGGTGGCC	ATGATCCAGG	840
TCGACAAGGC	GCTCAACGAG	GCACAGCTGG	CGTCGCGCAT	GCTGCTGCAG	GTCCACGACG	900
AGCTGCTGTT	CGAAATCGCC	CCCAGTGAAC	GCGAGCGGGT	CGAGGCCCTG	GTGCGCGACA	960
AGATGGGCGG	CGCTTACCCG	CTCGACGTCC	CGCTGGAGGT	GTCGGTGGGC	TACGGCCGCA	1020
GCTGGGACGC	GGCGGCGCAC	TGAGTGCCGA	GCGTGATCT	GGGGCGGGAA	TTCGGCGATT	1080
TTTCCGCCCT	GAGTTCACGC	TCGGCGCAAT	CGGGACCGAG	TTTGTCCAGC	GTGTACCCGT	1140
CGAGTAGCCT	CGTCA					1155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCCGTC	TGGTGTTTGA	ACGGTTTTAC	CGGTCGGCAT	CGGCACGGGC	GTTGCCGGGT	60
TCGGGCTTCG	GGTTGGCGAT	CGTCAAACAG	GTGGTGCTCA	ACCACGGCGG	ATTGCTGCGC	120
ATCGAAGACA	CCGACCCAGG	CGGCCAGCCC	CCTGGAACGT	CGATTTACGT	GCTGCTCCCC	180
GGCCGTCGGA	TGCCGATTCC	GCAGCTTCCC	GGTGCGACGG	CTGGCGCTCG	GAGCACGGAC	240
ATCGAGAACT	CTCGGGGTTC	GGCGAACGTT	ATCTCAGTGG	AATCTCAGTC	CACGCGCGCA	300
ACCTAGTTGT	GCAGTTACTG	TTGAAAGCCA	CACCCATGCC	AGTCCACGCA	TGGCCAAGTT	360
GGCCCGAGTA	GTGGGCCTAG	TACAGGAAGA	GCAACCTAGC	GACATGACGA	ATCACCCACG	420
GTATTCGCCA	CCGCCGCAGC	AGCCGGGAAC	CCCAGGTTAT	GCTCAGGGGC	AGCAGCAAAC	480
GTACAGCCAG	CAGTTCGACT	GGCGTTACCC	ACCGTCCCCG	CCCCCGCAGC	CAACCCAGTA	540
CCGTCAACCC	TACGAGGCGT	TGGGTGGTAC	CCGGCCGGGT	CTGATACCTG	GCGTGATTCC	600

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GACCATGACG CCCCCCTCCTG GGATGGTTTCG CCAACGCCCT CGTGCAGGCA TGTGCGCCAT 660
 CGGCGCGGTG ACGATAGCGG TGGTGTCCGC CGGCATCGGC GGCGCGGCCG CATCCCTGGT 720
 CGGGTTCAAC CGGGCACCCG CCGGCCCCAG CGGCGGCCCA GTGGCTGCCA GCGCGGCGCC 780
 AAGCATCCCC GCAGCAAACA TGCCGCCGGG GTCGGTCGAA CAGGTGGCGG CCAAGGTGGT 840
 GCCCAGTGTC GTCATGTTGG AAACCGATCT GGGCCGCCAG TCGGAGGAGG GCTCCGGCAT 900
 CATTCTGTCT GCCGAGGGGC TGATCTTGAC CAACAACCAC GTGATCGCGG CGGCCGCCAA 960
 GCCTCCCCTG GGCAGTCCGC CGCCGAAAAC GACGGTAACC TTCTCTGACG GCGCGACCGC 1020
 ACCCTTCACG GTGGTGGGGG CTGACCCAC CAGTGATATC GCCGTCGTCC GTGTTTCAGG 1080
 CGTCTCCGGG CTCACCCCGA TCTCCCTGGG TTCCTCCTCG GACCTGAGGG TCGGTCAGCC 1140
 GGTGCTGGCG ATCGGGTCGC CGCTCGGTTT GGAGGGCACC GTGACCACGG GGATCGTCAG 1200
 CGCTCTCAAC CGTCCAGTGT CGACGACCGG CGAGGCCCGG AACCAGAACCA CCGTGCTGGA 1260
 CGCCATTGAG ACCGACGCCG CGATCAACCC CGGTAACCTC GGGGGCGCGC TGGTGAACAT 1320
 GAACGCTCAA CTCGTCGGAG TCAACTCGGC CATTGCCACG CTGGGCGCGG ACTCAGCCGA 1380
 TGCGCAGAGC GGCTCGATCG GTCTCGGTTT TGCGATTCCA GTCGACCAGG CCAAGCGCAT 1440
 CGCCGACGAG TTGATCAGCA CCGGCAAGGC GTCACATGCC TCCCTGGGTG TGCAGGTGAC 1500
 CAATGACAAA GACACCCCGG GCGCCAAGAT CGTCGAAGTA GTGGCCGGTG GTGTCGCCG 1560
 GAACGCTGGA GTGCCGAAGG GCGTCGTTGT CACCAAGGTC GACGACCGCC CGATCAACAG 1620
 CGCGGACCGG TTGGTTGCCG CCGTGCGGTC CAAAGCGCCG GGCGCCACGG TGGCGCTAAC 1680
 CTTTCAGGAT CCCTCGGGCG GTAGCCGCAC AGTGCAAGTC ACCCTCGGCA AGGCGGAGCA 1740
 GTGATGAAGG TCGCCGCGCA GTGTTCAAAG C 1771

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCGCG GTGGCGGCCG CTCTAGAACT AGTGGATCCC CCGGGCTGCA GGAATTCGGC 60
 ACGAGGATCC GACGTCGCAG GTTGTGCAAC CCGCCGCCGC GGAAGTATCG GTCCATGCCT 120
 AGCCCGGCGA CGGCGAGCGC CGGAATGGCG CGAGTGAGGA GGCGGGCAAT TTGGCGGGGC 180
 CCGGCGACGG CGAGCGCCGG AATGGCGCGA GTGAGGAGGC GGGCAGTCAT GCCCAGCGTG 240
 ATCCAATCAA CCTGCATTGCG GCCTGCGGGC CCATTTGACA ATCGAGGTAG TGAGCGCAA 300
 TGAATGATGG AAAACGGGCG GTGACGTCCG CTGTTCTGGT GGTGCTAGGT GCCTGCCTGG 360
 CGTTGTGGCT ATCAGGATGT TCTTCGCCGA AACCTGATGC CGAGGAACAG GGTGTTCCCG 420
 TGAGCCCGAC GCGTCCGAC CCCGCGCTCC TCGCCGAGAT CAGGCAGTCG CTTGATGCGA 480
 CAAAAGGGTT GACCAGCGTG CACGTAGCGG TCCGAACAAC CGGAAAGTC GACAGCTTGC 540
 TGGGTATTAC CAGTGCCGAT GTCGACGTCC GGGCCAATCC GCTCGCGGCA AAGGGCGTAT 600
 GCACCTACAA CGACGAGCAG GGTGTCCCGT TTCGGGTACA AGGCGACAAC ATCTCGGTGA 660
 AACTGTTTCA CGACTGGAGC AATCTCGGCT CGATTTCTGA ACTGTCAACT TCACGCGTGC 720
 TCGATCCTGC CGCTGGGGTG ACGCAGCTGC TGTCCGGTGT CACGAACCTC CAAGCGCAAG 780
 GTACCGAAGT GATAGACGGA ATTTGACCA CAAAATCAC CGGGACCATC CCCGCGAGCT 840
 CTGTCAAGAT GCTTGATCCT GGCGCCAAGA GTGCAAGGCC GGCGACCGTG TGGATTGCCC 900
 AGGACGGCTC GCACCACCTC GTCCGAGCGA GCATCGACCT CGGATCCGGG TCGATTGAGC 960
 TCACGCGATC GAAATGGAAC GAACCCGTCA ACGTCGACTA GGCCGAAGTT GCGTCGACGC 1020
 GTTGNTCGAA ACGCCCTTGT GAACGGTGTC AACGGNAC 1058

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
 (B) TYPE: nucleic acid

10084843.022502

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA	CGAGAGGTGA	TCGACATCAT	CGGGACCAGC	CCCACATCGT	GGGAACAGGC	60
GGCGGCGGAG	GCGGTCCAGC	GGGCGCGGGA	TAGCGTCGAT	GACATCCGCG	TCGCTCGGGT	120
CATTGAGCAG	GACATGGCCG	TGGACAGCGC	CGGCAAGATC	ACCTACCGCA	TCAAGCTCGA	180
AGTGTCGTTT	AAGATGAGGC	CGGCGCAACC	GCGCTAGCAC	GGGCCGGCGA	GCAAGACGCA	240
AAATCGCACG	GTTTGCGGTT	GATTCGTGCG	ATTTTGTGTC	TGCTCGCCGA	GGCCTACCAG	300
GCGCGGCCCA	GGTCCGCGTG	CTGCCGTATC	CAGGCGTGCA	TCGCGATTCC	GGCGGCCACG	360
CCGGAGTTAA	TGCTTCGCGT	CGACCCGAAC	TGGGCGATCC	GCCGNGAGC	TGATCGATGA	420
CCGTGGCCAG	CCCGTCGATG	CCCGAGTTGC	CCGAGGAAAC	GTGCTGCCAG	GCCGGTAGGA	480
AGCGTCCGTA	GGCGGCGGTG	CTGACCGGCT	CTGCCTGCGC	CCTCAGTGCG	GCCAGCGAGC	540
GG						542

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 913 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCCGCC	CGCGCCTCCG	TGCCCCCAT	TGCCGCCGTC	GCCGATCAGC	TGCGCATCGC	60
CACCATCACC	GCCTTTGCCG	CCGGCACC GC	CGGTGGCGCC	GGGGCCGCCG	ATGCCACCGC	120
TTGACCCTGG	CCGCCGGCGC	CGCCATTGCC	ATACAGCACC	CCGCCGGGGG	CACCGTTACC	180
GCCGTCGCCA	CCGTCGCCGC	CGCTGCCGTT	TCAGGCCGGG	GAGGCCGAAT	GAACCGCCGC	240
CAAGCCCGCC	GCCGGCACCG	TGCGCGCCTT	TTCCGCCCGC	CCCGCCGGCG	CCGCCAATTG	300
CCGAACAGCC	AMGCACCGTT	GCCGCCAGCC	CCGCCGCCGT	TAACGGCGCT	GCCGGGCGCC	360
GCCGCCGGAC	CCGCCATTAC	CGCCGTTCCC	GTTCCGGTGCC	CCGCCGTTAC	CGGCGCCGCC	420
GTTTGCCGCC	AATATTCGGC	GGGCACCGCC	AGACCCGCCG	GGGCCACCAT	TGCCGCCGGG	480
CACCGAAACA	ACAGCCCAAC	GGTGCCGCCG	GCCCCGCCGT	TTGCCGCCAT	CACCGGCCAT	540
TCACCGCCAG	CACCGCCGTT	AATGTTTATG	AACCCGGTAC	CGCCAGCGCG	GCCCCTATTG	600
CCGGGCGCCG	GAGNGCGTGC	CCGCCGGCGC	CGCCAACGCC	CAAAAGCCCG	GGGTGCCAC	660
CGGCCCCGCC	GGACCCACCG	GTCCCGCCGA	TCCCCCGGTT	GCCGCCGGTG	CCGCCGCCAT	720
TGGTGCTGCT	GAAGCCGTTA	GCGCCGGTTC	CGCSGGTTCC	GGCGGTGGCG	CCNTGGCCGC	780
CGGCCCCGCC	GTTGCCGTAC	AGCCACCCCC	CGGTGGCGCC	GTTGCCGCCA	TTGCCGCCAT	840
TGCCGCCGTT	GCCGCCATTG	CCGCCGTTCC	CGCCGCCACC	GCCGGNTTGG	CCGCCGGCGC	900
CGCCGGCGGC	CGC					913

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG	GTGTAGAAAA	ATCCTGCCGC	CCGGACCCTT	AAGGCTGGGA	CAATTTCTGA	60
TAGCTACCCC	GACACAGGAG	GTTACGGGAT	GAGCAATTCT	CGCCGCCGCT	CACTCAGGTG	120

GTCATGGTTG CTGAGCGTGC TGGCTGCCGT CGGGCTGGGC CTGGCCACGG CGCCGGCCCA 180
 GGCGGCCCCG CCGGCCTTGT CGCAGGACCG GTTCGCCGAC TTCCCCGCGC TGCCCCCTGA 240
 CCCGTCCGCG ATGGTCGCCC AAGTGGCGCC ACAGGTGGTC AACATCAACA CCAAACCTGG 300
 CTACAACAAC GCCGTGGGCG CCGGGACCGG CATCGTCATC GATCCCAACG GTGTCTGTCT 360
 GACCAACAAC CACGTGATCG CGGGCGCCAC CGACATCAAT GCGTTCAGCG TCGGCTCCGG 420
 CCAAACCTAC GCGTCGATG TGGTCGGGTA TGACCGCACC CAGGATGTCT CCGTGCTGCA 480
 GCTGCGCGGT GCCGGTGGCC TGCCGTCGGC GCGGATCGGT GGCGGCGTCG CCGTTGGTGA 540
 GCGCGTCGTC GCGATGGGCA ACAGCGGTGG GCAGGGCGGA ACGCCCCGTG CCGTGCTTGG 600
 CAGGGTGGTC GCGCTCGGCC AAACCGTGCA GGCGTCGGAT TCGCTGACCG GTGCCGAAGA 660
 GACATTGAAC GGGTTGATCC AGTTCGATGC CGCAATCCAG CCCGGTGATT CCGGCGGGCC 720
 CGTCGTCAAC GGCCTAGGAC AGGTGGTCCG TATGAACACG GCCGCGTCCG ATAACCTCCA 780
 GCTGTCCAG GGTGGGCAGG GATTCGCCAT TCCGATCGGG CAGGCGATGG CGATCGCGGG 840
 CCAAATCCGA TCGGGTGGGG GGTCAACCCG CGTTTCATATC GGGCCTACCG CCTTCTCCG 900
 CTTGGGTGTT GTCGACAACA ACGGCAACGG CGCACGAGTC CAACGCGTGG TCGGAAGCGC 960
 TCCGGCGGCA AGTCTCGGCA TCTCCACCGG CGACGTGATC ACCGCGGTCTG ACGGCGCTCC 1020
 GATCAACTGG GCGACCGCGA TGGCGGACGC GCTTAACGGG CATCATCCCG GTGACGTCAT 1080
 CTCGGTGAAC TGGCAAACCA AGTCGGGCGG CACGCGTACA GGAACGTGA CATTGGCCGA 1140
 GGGACCCCCG GCCTGATTG TCGCGGATAC CACCGCCGG CCGGCCAATT GGATTGGCGC 1200
 CAGCCGTGAT TGCCGCGTGA GCGCCGAGT TCCGTCTCCC GTGCGCGTGG CATTGTGGAA 1260
 GCAATGAACG AGGCAGAACA CAGCGTTGAG CACCCTCCCG TGCAGGGCAG TTACGTCGAA 1320
 GGCGGTGTGG TCGAGCATCC GGATGCCAAG GACTTCGGCA GCGCCGCCGC CCTGCCCGCC 1380
 GATCCGACCT GGTTTAAGCA CGCCGTCTTC TACGAGGTGC TGGTCCGGGC GTTCTTCGAC 1440
 GCCAGCGCGG ACGGTTCCGN CGATCTGCGT GGACTCATCG ATCGCCTCGA CTACCTGCAG 1500
 TGGCTTGGCA TCGACTGCAT CTGTTGCCGC CGTTCCTACG ACTCACCGCT GCGCGACGGC 1560
 GGTTACGACA TTCGCGACTT CTACAAGGTG CTGCCCGAAT TCGGCACCGT CGACGATTC 1620
 GTCGCCCTGG TCGACACCGC TCACCGGCGA GGTATCCGCA TCATCACCGA CCTGGTGATG 1680
 AATCACACCT CGGAGTCGCA CCCCTGGTTT CAGGAGTCCC GCCGCGACCC AGACGGACCG 1740
 TACGGTGACT ATTACGTGTG GAGCGACACC AGCGAGCGCT ACACCGACGC CCGGATCATC 1800
 TTCGTCGACA CCGAAGAGTC GAACTGGTCA TTCGATCCTG TCCGCCGACA GTTNCCTACTG 1860
 GCACCGATTC TT 1872

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCCGCCGA ACCTGATGCC GAGGAACAGG GTGTTCCCGT GAGCCCGACG GCGTCCGACC 60
 CCGCGCTCCT CGCCGAGATC AGGCAGTCGC TTGATGCGAC AAAAGGGTTG ACCAGCGTGC 120
 ACGTAGCGGT CCGAACAACC GGGAAAGTCG ACAGCTTGCT GGGTATTACC AGTGCCGATG 180
 TCGACGTCCG GGCCAATCCG CTCGCGGCAA AGGGCGTATG CACCTACAAC GACGAGCAGG 240
 GTGTCCCGTT TCGGGTACAA GGCAGACAAC TCTCGGTGAA ACTGTTTCGAC GACTGGAGCA 300
 ATCTCGGCTC GATTTCTGAA CTGTCAACTT CACGCGTGCT CGATCCTGCC GCTGGGGTGA 360
 CGCAGCTGCT GTCCGGTGTC ACGAACCTCC AAGCGCAAGG TACCGAAGTG ATAGACGGAA 420
 TTTGACACAC CAAATCACC GGGACCATCC CCGCGAGCTC TGTCAAGATG CTTGATCCTG 480
 GCGCCAAGAG TGCAAGGCCG GCGACCGTGT GGATTGCCCA GGACGGCTCG CACCACCTCG 540
 TCCGAGCGAG CATCGACCTC GGATCCGGGT CGATTGAGCT CACGCGATCG AAATGGAACG 600
 AACCCGTCAA CGTCGACTAG GCCGAAGTTG CGTCGACGCG TTGCTCGAAA CGCCCTTGTG 660
 AACGGTGTCA ACGGCACCCG AAAACTGACC CCCTGACGGC ATCTGAAAAT TGACCCCTTA 720
 GACCGGGCGG TTGGTGGTTA TTCTTCGGTG GTTCCGGCTG GTGGGACGCG GCCGAGGTCTG 780
 CGGTCTTTGA GCCGGTAGCT GTCGCCCTTG AGGGCGACGA CTTGAGCATG GTGGACGAGG 840

CGGTTCGATCA	TGGCGGCAGC	AACGACGTCG	TCGCCGCCGA	AAACCTCGCC	CCACCGGCCG	900
AAGGCCTTAT	TGGACGTGAC	GATCAAGCTG	GCCCGCTCAT	ACCGGGAGGA	CACCAGCTGG	960
AAGAAGAGGT	TGGCGGCCTC	GGGCTCAAAC	GGAATGTAAC	CGACTTCGTC	AACCACCAGG	1020
AGCGGATAGC	GGCCAAACCG	GGTGAGTTCG	GCGTAGATGC	GCCCGGCGTG	GTGAGCCTCG	1080
GCGAACCGTG	CTACCCATTC	GGCGGCGGTG	GCGAACAGCA	CCCGATGACC	GGCCTGACAC	1140
GCGCGTATCG	CCAGGCCGAC	CGCAAGATGA	GTCTTCCCGG	TGCCAGGCGG	GGCCCAAAAA	1200
CACGACGTTA	TCGCGGGCGG	TGATGAAATC	CAGGGTGCCC	AGATGTGCGA	TGGTGTGCGG	1260
TTTGAGGCCA	CGAGCATGCT	CAAAGTCGAA	CTCTTCCAAC	GACTTCCGAA	CCGGGAAGCG	1320
GGCGGCGCGG	ATGCGGCCCT	CACCACCATG	GGACTCCCGG	GCTGACACTT	CCCGCTGCAG	1380
GCAGGCGGCC	AGGTATTCTT	CGTGGCTCCA	GTTCTCGGCG	CGGGCGCGAT	CGGCCAGCCG	1440
GGACACTGAC	TCACGCAGGG	TGGGAGCTTT	CAATGCTCTT	GT		1482

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA	CGAGCCGGCG	ATAGCTTCTG	GGCCGCGGCC	GACCAGATGG	CTCGAGGGTT	60
CGTGCTCGGG	GCCACCGCCG	GGCGCACCAC	CCTGACCGGT	GAGGGCCTGC	AACACGCCGA	120
CGGTCACTCG	TTGCTGCTGG	ACGCCACCAA	CCCGGCGGTG	GTTGCCTACG	ACCCGGCCTT	180
CGCCTACGAA	ATCGGCTACA	TCNGGAAAG	CGGACTGGCC	AGGATGTGCG	GGGAGAACCC	240
GGAGAACATC	TTCTTCTACA	TCACCGTCTA	CAACGAGCCG	TACGTGCAGC	CGCCGGAGCC	300
GGAGAACTTC	GATCCCGAGG	GCGTGCTGGG	GGGTATCTAC	CGNTATCACG	CGGCCACCGA	360
GCAACGCACC	AACAAGNGC	AGATCCTGGC	CTCCGGGGTA	GCGATGCCCG	CGGCGCTGCG	420
GGCAGCACAG	ATGCTGGCCG	CCGAGTGGGA	TGTCGCCGCC	GACGTGTGGT	CGGTGACCAG	480
TTGGGCGCAG	CTAAACCGCG	ACGGGTGGT	CATCGAGACC	GAGAAGCTCC	GCCACCCCGA	540
TCGGCCGGCG	GGCGTGCCCT	ACGTGACGAG	AGCGCTGGAG	AATGCTCGGG	GCCCAGTGAT	600
CGCGGTGTCG	GACTGGATGC	GCGCGGTCCC	CGAGCAGATC	CGACCGTGGG	TGCCGGGCAC	660
ATACCTCACG	TTGGGCACCG	ACGGGTTCGG	TTTTTCCGAC	ACTCGGCCCG	CCGGTCTGTCG	720
TTACTTCAAC	ACCGACGCCG	AATCCAGGT	TGGTCGCGGT	TTTGGGAGGG	GTTGGCCGGG	780
TCGACGGGTG	AATATCGACC	CATTGCGTGC	CGGTGCTGGG	CCGCCCCGCC	AGTTACCCGG	840
ATTCGACGAA	GGTGGGGGGT	TGCGCCCGAN	TAAGTT			876

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGCG	GCTGCAGGAA	TTCGGCACGA	GAGACAAAAT	TCCACGCGTT	AATGCAGGAA	60
CAGATTCATA	ACGAATTCAC	AGCGGCACAA	CAATATGTCG	CGATCGCGGT	TTATTTTCGAC	120
AGCGAAGACC	TGCCGCAGTT	GGCGAAGCAT	TTTTACAGCC	AAGCGGTCGA	GGAACGAAAC	180
CATGCAATGA	TGCTCGTGCA	ACACCTGCTC	GACCGCGACC	TTCGTGTCGA	AATTCCTGGC	240
GTAGACACGG	TGCGAAACCA	GTTGACAGAG	CCCCGCGAGG	CACTGGCGCT	GGCGCTCGAT	300
CAGGAACGCA	CAGTCACCGA	CCAGGTCGGT	CGGCTGACAG	CGGTGGCCCG	CGACGAGGGC	360
GATTCCTCG	GCGAGCAGTT	CATGCAGTGG	TTCTTGACAG	AACAGATCGA	AGAGGTGGCC	420

TTGATGGCAA	CCCTGGTGCG	GGTTGCCGAT	CGGGCCGGGG	CCAACCTGTT	CGAGCTAGAG	480
AACTTCGTCG	CACGTGAAGT	GGATGTGGCG	CCGGCCGCAT	CAGGCGCCCC	GCACGCTGCC	540
GGGGGCCGCC	TCTAGATCCC	TGGGGGGGAT	CAGCGAGTGG	TCCCGTTCGC	CCGCCCCGTCT	600
TCCAGCCAGG	CCTTGGTGCG	GCCGGGGTGG	TGAGTACCAA	TCCAGGCCAC	CCCAGCTTCC	660
CGGNAAAAGT	CGATGTCCTC	GTACTCATCG	ACGTTCCAGG	AGTACACCGC	CCGGCCCTGA	720
GCTGCCGAGC	GGTCAACGAG	TTGCGGATAT	TCCTTTAACG	CAGGCAGTGA	GGGTCCCACG	780
GCGGTTGGCC	CGACCGCCGT	GGCCGCACTG	CTGGTCAGGT	ATCGGGGGGT	CTTGGCGAGC	840
AACAACGTCG	GCAGGAGGGG	TGGAGCCCGC	CGGATCCGCA	GACCGGGGGG	GCGAAAACGA	900
CATCAACACC	GCACGGGATC	GATCTGCGGA	GGGGGGTGCG	GGAATACCGA	ACCGGTGTAG	960
GAGCGCCAGC	AGTTGTTTTT	CCACCAGCGA	AGCGTTTTTC	GGTCATCGGN	GGCNNTTAAG	1020
T						1021

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGCCGACG	AACGGAAGAA	CACAACCATG	AAGATGGTGA	AATCGATCGC	CGCAGGTCTG	60
ACCGCCGCGG	CTGCAATCGG	CGCCGCTGCG	GCCGGTGTGA	CTTCGATCAT	GGCTGGCGGN	120
CCGGTCGTAT	ACCAGATGCA	GCCGGTCGTC	TTCGGCGCGC	CACTGCCGTT	GGACCCGGNA	180
TCCGCCCCTG	ANGTCCCGAC	CGCCGCCCCAG	TGGACCAGNC	TGCTCAACAG	NCTCGNCGAT	240
CCCAACGTGT	CGTTTNGNAA	CAAGGGNAGT	CTGGTCGAGG	GNGGNATCGG	NGGNANCGAG	300
GGNGNGNATC	GNCGANACA	A				321

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT	TCCGGTTGGC	GACGGGTTTT	GGGNGCGGGT	GGTTAACCCG	CTCGGCCAGC	60
CGATCGACGG	GCGCGGAGAC	GTCGACTCCG	ATACTCGGCG	CGCGCTGGAG	CTCCAGGCGC	120
CCTCGGTGGT	GNACCGGCAA	GGCGTGAAGG	AGCCGTTGNA	GACCGGGATC	AAGGCGATTG	180
ACGCGATGAC	CCCGATCGGC	CGCGGGCAGC	GCCAGCTGAT	CATCGGGGAC	CGCAAGACCG	240
GCAAAAACCG	CCGTCTGTGT	CGGACACCAT	CCTCAAACCA	GCGGGAAGAA	CTGGGAGTCC	300
GGTGGATCCC	AAGAAGCAGG	TGCGCTTGTG	TATACGTTGG	CCATCGGGCA	AGAAGGGGAA	360
CTTACCATCG	CCG					373

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACGCCGT	GATGGGATTC	CTGGGCGGGG	CCGGTCCGCT	GGCGGTGGTG	GATCAGCAAC	60
TGGTTACCCG	GGTGCCGCAA	GGCTGGTCGT	TTGCTCAGGC	AGCCGCTGTG	CCGGTGGTGT	120
TCTTGACGGC	CTGGTACGGG	TTGGCCGATT	TAGCCGAGAT	CAAGGCGGGC	GAATCGGTGC	180
TGATCCATGC	CGGTACCGGC	GGTGTGGGCA	TGGCGGCTGT	GCAGCTGGCT	CGCCAGTGGG	240
GCGTGGAGGT	TTTCGTCACC	GCCAGCCGTG	GNAAGTGGGA	CACGCTGCGC	GCCATNGNGT	300
TTGACGACGA	NCCATATCGG	NGATTCCNC	ACATNCGAAG	TTCCGANGGA	GA	352

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCGCG	TTCATTCCGT	TCGACCAGCG	GCTGGCGATA	ATCGACGAAG	TGATCAAGCC	60
GCGGTTTCGCG	GCGCTCATGG	GTCACAGCGA	GTAATCAGCA	AGTTCTCTGG	TATATCGCAC	120
CTAGCGTCCA	GTTGCTTGCC	AGATCGCTTT	CGTACCGTCA	TCGCATGTAC	CGGTTCGCGT	180
GCCGCACGCT	CATGCTGGCG	GCGTGCATCC	TGGCCACGGG	TGTGGCGGGT	CTCGGGGTCG	240
GCGCGCAGTC	CGCAGCCCAA	ACCGCGCCGG	TGCCCGACTA	CTACTGGTGC	CCGGGGCAGC	300
CTTTCGACCC	CGCATGGGGG	CCCAACTGGG	ATCCCTACAC	CTGCCATGAC	GACTTCCACC	360
GCGACAGCGA	CGGCCCCGAC	CACAGCCGCG	ACTACCCCGG	ACCCATCCTC	GAAGGTCCCC	420
TGCTTGACGA	TCCCCGTGCT	GCGCCGCCGC	CCCCGGCTGC	CGGTGGCGGC	GCATAGCGCT	480
CGTTGACCGG	CGCGCATCAG	CGAATACGCG	TATAAACCCG	GGCGTGCCCC	CGGCAAGCTA	540
CGACCCCCGG	CGGGGCAGAT	TTACGCTCCC	GTGCCGATGG	ATCGCGCCGT	CCGATGACAG	600
AAAATAGGCG	ACGGTTTTTG	CAACCGCTTG	GAGGACGCTT	GAAGGGAACC	TGTCATGAAC	660
GGCGACAGCG	CCTCCACCAT	CGACATCGAC	AAGGTTGTTA	CCCGCACACC	CGTTCGCCGG	720
ATCGTG						726

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGACG	ACGAACGTCG	GGCCCCACCAC	CGCCTATGCG	TTGATGCAGG	CGACCGGGAT	60
GGTCGCCGAC	CATATCCAAG	CATGCTGGGT	GCCCACTGAG	CGACCTTTTG	ACCAGCCGGG	120
CTGCCCGATG	GCGGCCCGGT	GAAGTCATTG	CGCCGGGGCT	TGTGCACCTG	ATGAACCCGA	180
ATAGGGAACA	ATAGGGGGGT	GATTTGGCAG	TTCAATGTCG	GGTATGGCTG	GAAATCCAAT	240
GGCGGGGCAT	GCTCGGCGCC	GACCAGGCTC	GCGCAGGCGG	GCCAGCCCGA	ATCTGGAGGG	300
AGCACTCAAT	GGCGGCGATG	AAGCCCCGGA	CCGGCGACGG	TCCTTTGGAA	GCAACTAAGG	360
AGGGGCGCGG	CATTGTGATG	CGAGTACCAC	TTGAGGGTGG	CGGTCGCCTG	GTCGTCGAGC	420
TGACACCCGA	CGAAGCCGCC	GCACTGGGTG	ACGAACTCAA	AGGCGTTACT	AGCTAAGACC	480
AGCCCAACGG	CGAATGGTCG	GCGTTACGCG	CACACCTTCC	GGTAGATGTC	CAGTGTCTGC	540
TCGGCGATGT	ATGCCCAGGA	GAACTCTTGG	ATACAGCGCT			580

(2) INFORMATION FOR SEQ ID NO:26:

205220" E484800T

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGGCG CCGGGGGTTT TGGCGGGGCC GGGGCGGTTCG GCGGCAACGG CGGGGCCGGC	60
GGTACCGCCG GGTTGTTCCG TGTCGGCGGG GCCGGTGGGG CCGGAGGCAA CGGCATCGCC	120
GGTGTACGG GTACGTCGGC CAGCACACCG GGTGGATCCG	160

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCGATA CGATGGTGAT GTACGCCAAC GTTGTGACGA CGCTCGAGGC GTTCACGATC	60
CAGCGCACAC CCGACGGCGT GACCATCGGC GATGCGGCC CGTTCGCGGA GCGGGCTGCC	120
AAGGCGATGG GAATCGACAA GCTGCGGGTA ATTCATACCG GAATGGACCC CGTCGTCGCT	180
GAACGCGAAC AGTGGGACGA CGGCAACAAC ACGTTGGCGT TGGCGCCCGG TGTCGTTGTC	240
GCCTACGAGC GCAACGTACA GACCAACGCC CG	272

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCAGCCGGTG GTTCTCGGAC TATCTGCGCA CCGTGACGCA GCGCGACGTG CGCGAGCTGA	60
AGCGGATCGA GCAGACGGAT CGCCTGCCGC GGTTCATGCG CTACCTGGCC GCTATCACCG	120
CGCAGGAGCT GAACGTGGCC GAAGCGGCGC GGGTCATCGG GGTGACGCG GGGACGATCC	180
GTTCCGATCT GCGGTGGTTC GAGACGGTCT ATCTGGTACA TCGCCTGCCC GCCTGGTCGC	240
GGAATCTGAC CGCGAAGATC AAGAAGCGGT CAAAGATCCA CGTCGTCGAC AGTGGCTTCG	300
CGGCCTGGTT GCGCGGG	317

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

205220" E4848001

GATCGTGGAG	CTGTTCGATGA	ACAGCGTTGC	CGGACGCGCG	GCGGCCAGCA	CGTCGGTGTA	60
GCAGCGCCGG	ACCACCTCGC	CGGTGGGCAG	CATGGTGATG	ACCACGTCGG	CCTCGGCCAC	120
CGCTTCGGGC	GCGCTACGAA	ACACCGCGAC	ACCGTGC GCG	GCGGCGCCGG	ACGCCGCCGT	180
GG						182

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGCGAAG	TTTGGTGAGC	AGGTGGTCGA	CGCGAAAGTC	TGGGCGCCTG	CGAAGCGGGT	60
CGGCGTTTAC	GAGGCGAAGA	CACGCCTGTC	CGAGCTGCTG	CGGCTCGTCT	ACGGCGGGCA	120
GAGGTTGAGA	TTGCCCCCGG	CGGCGAGCCG	GTAGCAAAGC	TTGTGCCGCT	GCATCCTCAT	180
GAGACTCGGC	GGTTAGGCAT	TGACCATGGC	GTGTACCGCG	TGCCCCACGA	TTTGACGCT	240
CCGTTGTCAG	ACGACGTGCT	CGAACGCTTT	CACCGGTGAA	GCGCTACCTC	ATCGACACCC	300
ACGTTTGG						308

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGACGACGA	GCAACTCACG	TGGATGATGG	TCGGCAGCGG	CATTGAGGAC	GGAGAGAATC	60
CGGCCGAAGC	TGCCGCGCGG	CAAGTGCTCA	TAGTGACCGG	CCGTAGAGGG	CTCCCCGAT	120
GGCACCGGAC	TATTCTGGTG	TGCCGCTGGC	CGGTAAGAGC	GGGTAAAAGA	ATGTGAGGGG	180
ACACGATGAG	CAATCACACC	TACCGAGTGA	TCGAGATCGT	CGGGACCTCG	CCCCACGGCG	240
TCGACGCGGC	AATCCAGGGC	GGTCTGG				267

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGTGCCGA	AAGAATGTGA	GGGGACACGA	TGAGCAATCA	CACCTACCGA	GTGATCGAGA	60
TCGTGCGGGAC	CTCGCCCGAC	GGCGTCGACG	CGGCAATCCA	GGGCGGTCTG	GCCCCGAGCTG	120
CGCAGACCAT	GCGCGCGCTG	GA CTGGTTTCG	AAGTACAGTC	AATTTCGAGGC	CACCTGGTCTG	180
ACGGAGCGGT	CGCGCACTTC	CAGGTGACTA	TGAAAGTCGG	CTTCCGCTGG	AGGATTCCCTG	240
AACCTTCAAG	CGCGGCCGAT	AACTGAGGTG	CATCATTAAG	CGACTTTTCC	AGAACATCCT	300
GACGCGCTCG	AAACGCGGTT	CAGCCGACGG	TGGCTCCGCC	GAGGCGCTGC	CTCCAAAATC	360
CCTGCGACAA	TTGTCGGCG	GCGCCTACAA	GGAAGTCGGT	GCTGAATTCTG	TCGGGTATCT	420

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GGTCGACCTG	TGTGGGCTGC	AGCCGGACGA	AGCGGTGCTC	GACGTCGGCT	GCGGCTCGGG	480
GCGGATGGCG	TTGCCGCTCA	CCGGCTATCT	GAACAGCGAG	GGACGCTACG	CCGGCTTCGA	540
TATCTCGCAG	AAAGCCATCG	CGTGGTGCCA	GGAGCACATC	ACCTCGGCGC	ACCCCAACTT	600
CCAGTTCGAG	GTCTCCGACA	TCTACAACCTC	GCTGTACAAC	CCGAAAGGGA	AATACCAGTC	660
ACTAGACTTT	CGCTTTCCAT	ATCCGGATGC	GTCGTTTCGAT	GTGGTGTTC	TTACCTCGGT	720
GTTACCCAC	ATGTTTCCGC	CGGACGTGGA	GCACTATCTG	GACGAGATCT	CCCGCGTGCT	780
GAAGCCCGGC	GGACGATGCC	TGTGCACGTA	CTTCTTGCTC	AATGACGAGT	CGTTAGCCCA	840
CATCGCGGAA	GGAAAGAGTG	CGCACAACTT	CCAGCATGAG	GGACCGGGTT	ATCGGACAAT	900
CCACAAGAAG	CGGCCCGAAG	AAGCAATCGG	CTTGCCGGAG	ACCTTCGTCA	GGGATGTCTA	960
TGGCAAGTTC	GGCCTCGCCG	TGCACGAACC	ATTGCACTAC	GGCTCATGGA	GTGGCCGGGA	1020
ACCACGCCTA	AGCTTCCAGG	ACATCGTCAT	CGCGACCAA	ACCGCGAGCT	AGGTCGGCAT	1080
CCGGGAAGCA	TCGCGACACC	GTGGCGCCGA	GCGCCGCTGC	CGGCAGGCCG	ATTAGGCGGG	1140
CAGATTAGCC	CGCCGCGGCT	CCCGGCTCCG	AGTACGGCGC	CCCGAATGGC	GTCACCGGCT	1200
GGTAACCACG	CTTGCGCGCC	TGGGCGGCGG	CCTGCCGGAT	CAGGTGGTAG	ATGCCGACAA	1260
AGCCTGCGTG	ATCGGTCATC	ACCAACGGTG	ACAGCAGCCG	GTTGTGCACC	AGCGCGAACG	1320
CCACCCCGGT	CTCGGGGTCT	GTCCAGCCGA	TGAGCCGCC	CAGCCCAACA	TGACCAAAACC	1380
CCGGCATCAC	GTTGCCGATC	GGCATAACCGT	GATAGCCAAG	ATGAAAATTT	AAGGGCACCA	1440
ATAGATTTTCG	ATCCGGCAGA	ACTTGCCGTC	GGTTGCGGGT	CAGGCCCGTG	ACCAGCTCCC	1500
GCGACAAGAA	CCGTATGCCG	TCGATCTCGC	CTCGTGCCG			1539

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGTG	GCGTGGATGA	GCGTCACCGC	GGGGCAGGCC	GAGCTGACCG	CCGCCCAGGT	60
CCGGGTGCT	GCGGCGGCCT	ACGAGACGGC	GTATGGGCTG	ACGGTGCCCC	CGCCGGTGAT	120
CGCCGAGAAC	CGTGCTGAAC	TGATGATTCT	GATAGCGACC	AACCTCTTGG	GGCAAAACAC	180
CCCGGCGATC	GCGGTCAACG	AGGCCGAATA	CGGCGAGATG	TGGGCCCCAAG	ACGCCGCCGC	240
GATGTTTGGC	TACGCCGCGG	CGACGGCGAC	GGCGACGGCG	ACGTTGCTGC	CGTTCGAGGA	300
GGCGCCGGAG	ATGACCAGCG	CGGGTGGGCT	CCTCGAGCAG	GCCGCCGCGG	TCGAGGAGGC	360
CTCCGACACC	GCCGCGGCGA	ACCAGTTGAT	GAACAAATGTG	CCCCAGGCGC	TGAAACAGTT	420
GGCCCAGCCC	ACGCAGGGCA	CCACGCCTTC	TTCCAAGCTG	GGTGGCCTGT	GGAAGACGGT	480
CTCGCCGCAT	CGGTCGCCGA	TCAGCAACAT	GGTGTCGATG	GCCAACAACC	ACATGTCGAT	540
GACCAACTCG	GGTGTGTCGA	TGACCAACAC	CTTGAGCTCG	ATGTTGAAGG	GCTTTGCTCC	600
GGCGGCGGCC	GCCCAGGCCG	TGCAAACCGC	GGCGCAAAC	GGGGTCCGGG	CGATGAGCTC	660
GCTGGGCAGC	TCGCTGGGTT	CTTCGGGTCT	GGGCGGTGGG	GTGGCCGCCA	ACTTGGGTCTG	720
GGCGGCCTCG	GTACGGTATG	GTCACCGGGA	TGGCGGAAAA	TATGCANAGT	CTGGTCGGCG	780
GAACGGTGGT	CCGGCGTAAG	GTTTACCCCC	GTTTTCTGGA	TGCGGTGAAC	TTCGTCAACG	840
GAAACAGTTA	C					851

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGATCGG	GCGGAAATTT	GGACCAGATT	CGCCTCCGGC	GATAACCCAA	TCAATCGAAC	60
CTAGATTTAT	TCCGTCCAGG	GGCCCAGTA	ATGGCTCGCA	GGAGAGGAAC	CTTACTGCTG	120
CGGGCACCTG	TCGTAGGTCC	TCGATACGGC	GGAAGGCGTC	GACATTTTCC	ACCGACACCC	180
CCATCCAAAC	GTTCGAGGGC	CACTCCAGCT	TGTGAGCGAG	GCGACGCAGT	CGCAGGCTGC	240
GCTTGGTCAA	GATC					254

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCTGACC	GAAGCGGCCG	CCGCCAAGGC	GAAGTCGCTG	TTGGACCAGG	AGGGACGGGA	60
CGATCTGGCG	CTGCGGATCG	CGGTTTCAGC	GGGGGGGTGC	GCTGGATTGC	GCTATAACCT	120
TTTCTTCGAC	GACCGGACGC	TGGATGGTGA	CCAAACCGCG	GAGTTCGGTG	GTGTCAGGTT	180
GATCGTGGAC	CGGATGAGCG	CGCCGTATGT	GGAAGGCGCG	TCGATCGATT	TCGTCGACAC	240
TATTGAGAAG	CAAGGTTTAC	CATCGACAAT	CCCAACGCCA	CCGGCTCCTG	CGCGTGCGGG	300
GATTCGTTCA	ACTGATAAAA	CGTAGTACG	ACCCCGCGGT	GCGCAACACG	TACGAGCACA	360
CCAAGACCTG	ACCGCGCTGG	AAAAGCAACT	GAGCGATGCC	TTGCACCTGA	CCGCGTGGCG	420
GGCCGCCGGC	GGCAGGTGTC	ACCTGCATGG	TGAACAGCAC	CTGGGCCTGA	TATTGCGACC	480
AGTACACGAT	TTTGTCGATC	GAGGTCACCT	CGACCTGGGA	GAAGTCTTGG	CGGAACGCGT	540
CGCTGCTCAG	CTTGGCCAAG	GCCTGATCGG	AGCGCTTGTC	GCGCACGCCG	TCGTGGATAC	600
CGCACAGCGC	ATTGCGAACG	ATGGTGTCCA	CATCGCGGTT	CTCCAGCGCG	TTGAGGTATC	660
CCTGAATCCG	GGTTTGGGCC	GGTCCCTCCG	AGAATGTGCC	TGCCGTGTTG	GCTCCGTTGG	720
TGCGGACCCC	GTATATGATC	GCCGCCGTCA	TAGCCGACAC	CAGCGCGAGG	GCTACCACAA	780
TGCCGATCAG	CAGCCGCTTG	TGCCGTGCTG	TCGGGTAGGA	CACCTGCGGC	GGCACGCCGG	840
GATATGCGGC	GGGCGGCAGC	GCCGCGTCGT	CTGCCGGTCC	CGGGGCGAAG	GCCGGTTCCG	900
CGGCGCCGAG	GTCGTGGGGG	TAGTCCAGGG	CTTGGGGTTC	GTGGGATGAG	GGCTCGGGGT	960
ACGGCGCCGG	TCCGTTGGTG	CCGACACCGG	GGTTCGGCGA	GTGGGGACCG	GGCATTGTGG	1020
TTCTCCTAGG	GTGGTGGACG	GGACCAGCTG	CTAGGGCGAC	AACCGCCCGT	CGCGTCAGCC	1080
GGCAGCATCG	GCAATCAGGT	GAGCTCCCTA	GGCAGGCTAG	CGCAACAGCT	GCCGTCAGCT	1140
CTCAACGCGA	CGGGGCGGGC	CGCGGCGCCG	ATAATGTTGA	AAGACTAGGC	AACCTTAGGA	1200
ACGAAGGACG	GAGATTTTGT	GACGATC				1227

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

{xi} SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGGTGTCCG	CGGATCCGGC	GGGTGGTTGA	ACGGCAACGG	CGGGGCCGGC	GGGGCCGGCG	60
GGACCGGCGC	TAACGGTGGT	GCCGGCGGCA	ACGCCTGGTT	GTTCTGGGGC	GGCGGGTCCG	120
GCGGNGCCGG	CACCAATGGT	GGNGTCGGCG	GGTCCGGCGG	ATTGTCTAC	GGCAACGGCG	180
G						181

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGGTGTCGG	CGGATCCGGC	GGGTGGTTGA	ACGGCAACGG	CGGTGTCGGC	GGCCGGGGCG	60
GCGACGGCGT	CTTTGCCGGT	GCCGGCGGCC	AGGGCGGCCT	CGGTGGGCAG	GGCGGCAATG	120
GCGGCGGCTC	CACCGGCGGC	AACGGCGGTC	TTGGCGGCGC	GGGCGGTGGC	GGAGGCAACG	180
CCCCGGACGG	CGGCTTCGGT	GGCAACGGCG	GTAAGGGTGG	CCAGGGCGGN	ATTGGCGGCG	240
GCACTCAGAG	CGCGACCGGC	CTCGGNGGTG	ACGGCGGTGA	CGGCGGTGAC		290

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCCAGTGG	CATGGNGGGT	GTCAGTGGAA	GCAT	34
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(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGCTGCT	CGTCCCCCCC	TTGCCGCCGA	CGCCACCGGT	CCCACCGTTA	CCGAACAAGC	60
TGGCGTGGTC	GCCAGCACCC	CCGGCACCGC	CGACGCCGGA	GTCGAACAAT	GGCACCGTCG	120
TATCCCCACC	ATTGCCGCCG	GNCCCCACCG	CACCG			155

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGCGTTCA	CGGGGCGCCG	GGGACCGGGC	AGCCCGGNGG	GGCCGGGGGG	TGG	53
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(2) INFORMATION FOR SEQ ID NO:41:

205220 E4B4800T

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCACCGC GGGTGCAGAC GGTGCCCCGCG GCGCCACCCC GACCAGCGGC GGCAACGGCG	60
GCACCGGCGG CAACGGCGCG AACGCCACCG TCGTCGGNGG GGCCGGCGGG GCCGGCGGCA	120
AGGGCGGCAA CG	132

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGGCGGC CGGNACGGNC GGGGACGGCG GCAAGGGCGG NAACGGGGGC GCCGNAGCCA	60
CCNGCCAAGA ATCCTCCGNG TCCNCCAATG GCGCGAATGG CGGACAGGGC GGCAACGGCG	120
GCANCGGCGG CA	132

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC	60
CGAGGAAAGC CGCTACCAGA TGGCGTGCC GAAGTAGGGC GATCCGTTTCG CGATGCCGGC	120
ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTTCAGT TTAGCGACGA TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG	240
AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCAGATGGC GGACCCACCG ACTGATGTCC	300
CCATCACACC GTGCGAACTC ACGGNGGNTA AAAACGCCGC CCAACAGNTG GTNTTGTCCG	360
CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAGA GCGGCAGCGT CTGGCGACCT	420
CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG	480
ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCGG GGCCGTCGGA GGGGACAGTT	540
CGGCCGAAC TACCAGTACG CCGAGGGTGG CCACGGCCGG TGAACCAAC TTCATGGATC	600
TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGNG	660
GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCGA CG	702

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCCGCAG	CGCTGTCGGG	CGACGTGGCG	GTCAAAGCGG	CATCGCTCGG	TGGCGGTGGA	60
GGCGGCGGGG	TGCCGTCGGC	GCCGTTGGGA	TCCGCGATCG	GGGGCGCCGA	ATCGGTGCGG	120
CCCGCTGGCG	CTGGTGACAT	TGCCGGCTTA	GGCCAGGGAA	GGGCCGGCGG	CGGCGCCGCG	180
CTGGGCGGCG	GTGGCATGGG	AATGCCGATG	GGTGCCGCGC	ATCAGGGACA	AGGGGGCGCC	240
AAGTCCAAGG	GTTCTCAGCA	GGAAGACGAG	GCGCTCTACA	CCGAGGATCC	TCGTGCCG	298

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAGG	ATCGAATCGC	GTCGCCGGGA	GCACAGCGTC	GCACTGCACC	AGTGGAGGAG	60
CCATGACCTA	CTCGCCGGGT	AACCCCGGAT	ACCCGCAAGC	GCAGCCCGCA	GGCTCCTACG	120
GAGGCGTCAC	ACCCTCGTTC	GCCACGCCCG	ATGAGGGTGC	GAGCAAGCTA	CCGATGTACC	180
TGAACATCGC	GGTGGCAGTG	CTCGGTCTGG	CTGCGTACTT	CGCCAGCTTC	GGCCCAATGT	240
TCACCCCTCAG	TACCGAACTC	GGGGGGGGTG	ATGGCGCAGT	GTCCGGTGAC	ACTGGGCTGC	300
CGGTCCGGGT	GGCTCTGCTG	GCTGCGCTGC	TTGCCGGGGT	GGTTCTGGTG	CCTAAGGCCA	360
AGAGCCATGT	GACGGTAGTT	GCGGTGCTCG	GGGTACTCGG	CGTATTTCTG	ATGGTCTCGG	420
CGACGTTTAA	CAAGCCAGC	GCCTATTCTGA	CCGTTTGGGC	ATTGTGGGTT	GTGTTGGCTT	480
TCATCGTGTT	CCAGGCGGTT	GCGGCAGTCC	TGGCGCTCTT	GGTGGAGACC	GGCGCTATCA	540
CCGCGCCGGC	GCCGCGGCC	AAGTTCGACC	CGTATGGACA	GTACGGGCGG	TACGGGCAGT	600
ACGGGCAGTA	CGGGGTGCAG	CCGGGTGGGT	ACTACGGTCA	GCAGGGTGCT	CAGCAGGCCG	660
CGGGACTGCA	GTCGCCCCGC	CCGCAGCAGT	CTCCGCAGCC	TCCCGGATAT	GGGTGCGAGT	720
ACGGCGGCTA	TTCGTCCAGT	CCGAGCCAAT	CGGGCAGTGG	ATACACTGCT	CAGCCCCCGG	780
CCCAGCCGCC	GGCGCAGTCC	GGGTCGCAAC	AATCGCACCA	GGGCCCATCC	ACGCCACCTA	840
CCGGCTTTCC	GAGCTTCAGC	CCACCACCAC	CGGTCAGTGC	CGGGACGGGG	TCGCAGGCTG	900
GTTCGGCTCC	AGTCAACTAT	TCAAACCCCA	GCGGGGGCGA	GCAGTCGTCG	TCCCCCGGGG	960
GGGCGCCGGT	CTAACCGGGC	GTTCCCGCGT	CCGGTCGCGC	GTGTGCGCGA	AGAGTGAACA	1020
GGGTGTCAGC	AAGCGCGGAC	GATCCTCGTG	CCGAATTC			1058

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGAGA	GACCGATGCC	GCTACCCTCG	CGCAGGAGGC	AGGTAATTTT	GAGCGGATCT	60
CCGGCGACCT	GAAAACCCAG	ATCGACCAGG	TGGAGTCGAC	GGCAGGTTTC	TTGCAGGGCC	120
AGTGGCGCGG	CGCGGCGGGG	ACGGCCGCCC	AGGCCGCGGT	GGTGCGCTTC	CAAGAAGCAG	180
CCAATAAGCA	GAAGCAGGAA	CTCGACGAGA	TCTCGACGAA	TATTCGTCAG	GCCGGCGTCC	240
AATACTCGAG	GGCCGACGAG	GAGCAGCAGC	AGGCCGCTGTC	CTCGCAAATG	GGCTTCTGAC	300
CCGCTAATAC	GAAAAGAAAC	GGAGCAA				327

205220" Chaboot

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGTCGCGAT GATGGCGTTG TCGAACGTGA CCGATTCTGT ACCGCCGTCG TTGAGATCAA	60
CCAACAACGT GTTGGCGTCG GCAAATGTGC CGNACCCGTG GATCTCGGTG ATCTTGTTC	120
TCTTCATCAG GAAGTGCACA CCGGCCACCC TGCCCTCGGN TACCTTTCGG	170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGGCGG CACGGGGGGT GCCGGCGGCA GCACCGCTGG CGCTGGCGGC AACGGCGGGG	60
CCGGGGGTGG CGGCGGAACC GGTGGGTTGC TCTTCGGCAA CGGCGGTGCC GGCGGGCACG	120
GGGCCGT	127

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGCGGCAAG GGCGGCACCG CCGGCAACGG GAGCGGCGCG GCCGGCGGCA ACGGCGGCAA	60
CGGCGGCTCC GGCCTCAACG G	81

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGGCT GGCCGGCTCC GGCCAGAAGG GCGGTAACGG AGGAGCTGCC GGATTGTTTG	60
GCAACGGCGG GGCCGGNGGT GCCGGCGCGT CCAACCAAGC CGGTAACGGC GGNGCCGGCG	120
GAAACGGTGG TGCCGGTGGG CTGATCTGG	149

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACGAGA TCACACCTAC CGAGTGATCG AGATCGTCGG GACCTCGCCC GACGGTGTCTG	60
ACGCGGNAAT CCAGGGCGGT CTGGCCCAG CTGCGCAGAC CATGCGCGCG CTGGACTGGT	120
TCGAAGTACA GTCAATTCGA GGCCACCTGG TCGACGGAGC GGTCGCGCAC TTCCAGGTGA	180
CTATGAAAGT CGGCTTCCGC CTGGAGGATT CCTGAACCTT CAAGCGCGGC CGATAACTGA	240
GGTGCATCAT TAAGCGACTT TTCCAGAACA TCCTGACGCG CTGGAAAGCG GGTTCAGCCG	300
ACGGTGGCTC CGCCGAGGCG CTGCCTCCAA AATCCCTGCG ACAATTCGTC GGCGG	355

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACC ATCACCATCA CATGCATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA	60
CGATTGGCGG CACTGGCTAT CGCGGCGATG GCCAGCGCCA GCCTGGTGAC CGTTGCGGTG	120
CCCGCGACCG CCAACGCCGA TCCGGAGCCA GCGCCCCCGG TACCCACAAC GGCCGCCTCG	180
CCGCCGTGCA CCGCTGCAGC GCCACCCGCA CCGGCGACAC CTGTTGCCCC CCCACCACCG	240
GCCGCCGCCA ACACGCCGAA TGCCCAGCCG GCGGATCCCA ACGCAGCACC TCCGCCGGCC	300
GACCCGAACG CACCGCCGCC ACCTGTCAAT GCCCCAAACG CACCCCAACC TGTCCGGATC	360
GACAACCCGG TTGGAGGATT CAGCTTCGCG CTGCCTGCTG GCTGGGTGGA GTCTGACGCC	420
GCCCACTTCG ACTACGGTTC AGCACTCCTC AGCAAAACCA CCGGGGACCC GCCATTTCCTC	480
GGACAGCCGC CGCCGGTGGC CAATGACACC CGTATCGTGC TCGGCCGGCT AGACCAAAAG	540
CTTTACGCCA GCGCCGAAGC CACCGACTCC AAGGCCGCGG CCCGGTTGGG CTCGGACATG	600
GGTGAGTTCT ATATGCCCTA CCCGGGCACC CGGATCAACC AGGAAACCGT CTCGCTCGAC	660
GCCAACGGGG TGTCTGGAAG CGCGTCGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAAG	720
CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCTCGCCCG CGGCGAACGC ACCGGACGCC	780
GGGCCCCCTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAACCC GGTGGACAAG	840
GGCGCGGCCA AGGCGCTGGC CGAATCGATC CGGCCTTTGG TCGCCCCGCC GCCGGCGCCG	900
GCACCGGCTC CTGCAGAGCC CGCTCCGGCG CCGGCGCCCG CCGGGGAAGT CGCTCCTACC	960
CCGACGACAC CGACACCGCA GCGGACCTTA CCGGCCTGA	999

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

10034843 02502
205220 "Chaboot"

Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
 1 5 10 15
 Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
 20 25 30
 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
 35 40 45
 Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 50 55 60
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 65 70 75 80
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
 85 90 95
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
 100 105 110
 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
 115 120 125
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
 130 135 140
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
 145 150 155 160
 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
 165 170 175
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
 180 185 190
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 195 200 205
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 210 215 220
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
 225 230 235 240
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
 245 250 255
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
 260 265 270
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
 275 280 285
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
 290 295 300
 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
 305 310 315 320
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
 325 330

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val

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1	5	10	15
Val	Ala	Ala	Leu
	20		

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1				5					10						15
Glu	Gly	Arg													

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

10084843 022502
205220" C484800T

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
 1 5 10 15
 Ala

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
 1 5 10 15

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Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Glu Arg Lys
 1 5 10 15
 Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
 20 25 30
 Ala Ala Ala Ile Gly Ala Ala Ala Gly Val Thr Ser Ile Met Ala
 35 40 45
 Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
 50 55 60
 Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
 65 70 75 80
 Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
 85 90 95
 Asn Lys Gly Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg
 100 105 110
 Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
 115 120 125
 Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala
 130 135 140
 Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
 145 150 155 160
 Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
 165 170 175
 Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
 180 185

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
 1 5 10 15
 Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
 20 25 30
 Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
 35 40 45
 Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser

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50		55		60
Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val				
65		70		75
Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val				80
	85		90	
Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val				95
	100		105	
Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu				110
	115		120	
Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser				125
	130		135	
Thr Gly Gly Pro			140	
145				

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr				
1	5	10	15	
Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln				
	20	25	30	
Gln Arg Asp Ala Leu Cys Leu Ser Ser Thr Gln Ile Ser Arg Gln Ser				
	35	40	45	
Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn				
	50	55	60	
Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu				
65	70	75	80	
Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu				
	85	90	95	
Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser				
	100	105	110	
Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp				
	115	120	125	
Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu				
	130	135	140	
Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn				
145	150	155	160	
Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln				
	165	170	175	
Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr				
	180	185	190	
Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile				
	195	200	205	
Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val				
	210	215	220	
Phe Pro Ile Val Ala Arg				
225	230			

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(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1           5           10           15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20           25           30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35           40           45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50           55           60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65           70           75           80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85           90           95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100          105          110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115          120          125
Gly Pro Pro Ala
130

```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1           5           10           15
Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Arg Leu Ser Asn Pro Pro
20           25           30
Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35           40           45
Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
50           55           60
Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
65           70           75           80
Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
85           90           95
Ser Glu Arg Lys
100

```

(2) INFORMATION FOR SEQ ID NO:68:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1           5           10           15
Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20           25           30
Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
35           40           45
Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50           55           60
Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65           70           75           80
Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
85           90           95
Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
100          105          110
Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115          120          125
Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
130          135          140
His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
145          150          155          160
Asp Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
1           5           10           15
Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
20           25           30
Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
35           40           45
Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro
50           55           60
Arg Gly Arg Lys Glu Ala Val Ala Ala Val Ala Ala Ser Leu Arg
65           70           75           80
Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
85           90           95
Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
100          105          110

```

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Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
 115 120 125
 Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
 130 135 140
 Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
 145 150 155 160
 Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
 165 170 175
 Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
 180 185 190
 His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro
 195 200 205
 Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe
 210 215 220
 Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro
 225 230 235 240
 Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro
 245 250 255
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro
 260 265 270
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala
 275 280 285
 Pro His Gln Val Thr Asp Asp Val Ala Ala Ala Arg Ser Leu Leu
 290 295 300
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr
 305 310 315 320
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln
 325 330 335
 Val Ser Arg Gln Asn Pro Thr Gly
 340

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala
 1 5 10 15
 Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu
 20 25 30
 Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile
 35 40 45
 Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu
 50 55 60
 Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu
 65 70 75 80
 Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser
 85 90 95
 Thr Gly Glu Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Glu
 100 105 110

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Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala
 115 120 125
 Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met
 130 135 140
 Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro
 145 150 155 160
 Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala
 165 170 175
 Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu
 180 185 190
 Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly
 195 200 205
 Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
 210 215 220
 Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser
 225 230 235 240
 His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser
 245 250 255
 Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu
 260 265 270
 Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
 275 280 285
 Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
 290 295 300
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
 305 310 315 320
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
 325 330 335
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
 340 345 350
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
 355 360 365
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp
 370 375 380
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala
 385 390 395 400
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
 405 410 415
 Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
 420 425 430
 Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala
 435 440 445
 Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
 450 455 460
 Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
 465 470 475 480
 Val Ala Pro Thr Gly
 485

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
1      5      10      15
Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
20      25      30
Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
35      40      45
Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
50      55      60
Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
65      70      75      80
Gly Asn Ala Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro
85      90      95
Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
100     105     110
Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
115     120     125
Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
130     135     140
Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
145     150     155     160
Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
165     170     175
Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
180     185     190
Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
195     200     205
Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
210     215     220
Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
225     230     235     240
Gln Pro Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
245     250     255
Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly
260     265

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
1      5      10      15
Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
20      25      30
Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
35      40      45

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Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 50 55 60
 Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
 65 70 75 80
 Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu
 85 90 95
 Gln

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 364 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
 1 5 10 15
 Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
 20 25 30
 Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
 35 40 45
 Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
 50 55 60
 Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
 65 70 75 80
 Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
 85 90 95
 Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
 100 105 110
 Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
 115 120 125
 Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
 130 135 140
 Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro
 145 150 155 160
 Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile
 165 170 175
 Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
 180 185 190
 Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
 195 200 205
 Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
 210 215 220
 Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu
 225 230 235 240
 Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
 245 250 255
 Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
 260 265 270
 Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
 275 280 285
 Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile

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290		295		300
Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr				
305		310		315
Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly				320
	325		330	335
Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe				
	340		345	350
Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser				
355		360		

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln Ala Ala Ala Gly Arg Ala Val Arg Arg Thr Gly His Ala Glu Asp			
1	5	10	15
Gln Thr His Gln Asp Arg Leu His His Gly Cys Arg Arg Ala Ala Val			
	20	25	30
Val Val Arg Gln Asp Arg Ala Ser Val Ser Ala Thr Ser Ala Arg Pro			
	35	40	45
Pro Arg Arg His Pro Ala Gln Gly His Arg Arg Arg Val Ala Pro Ser			
	50	55	60
Gly Gly Arg Arg Arg Pro His Pro His His Val Gln Pro Asp Asp Arg			
65	70	75	80
Arg Asp Arg Pro Ala Leu Leu Asp Arg Thr Gln Pro Ala Glu His Pro			
	85	90	95
Asp Pro His Arg Arg Gly Pro Ala Asp Pro Gly Arg Val Arg Gly Arg			
	100	105	110
Gly Arg Leu Arg Arg Val Asp Asp Gly Arg Leu Gln Pro Asp Arg Asp			
	115	120	125
Ala Asp His Gly Ala Pro Val Arg Gly Arg Gly Pro His Arg Gly Val			
	130	135	140
Gln His Arg Gly Gly Pro Val Phe Val Arg Arg Val Pro Gly Val Arg			
145	150	155	160
Cys Ala His Arg Arg Gly His Arg Arg Val Ala Ala Pro Gly Gln Gly			
	165	170	175
Asp Val Leu Arg Ala Gly Leu Arg Val Glu Arg Leu Arg Pro Val Ala			
	180	185	190
Ala Val Glu Asn Leu His Arg Gly Ser Gln Arg Ala Asp Gly Arg Val			
	195	200	205
Phe Arg Pro Ile Arg Arg Gly Ala Arg Leu Pro Ala Arg Arg Ser Arg			
	210	215	220
Ala Gly Pro Gln Gly Arg Leu His Leu Asp Gly Ala Gly Pro Ser Pro			
225	230	235	240
Leu Pro Ala Arg Ala Gly Gln Gln Gln Pro Ser Ser Ala Gly Gly Arg			
	245	250	255
Arg Ala Gly Gly Ala Glu Arg Ala Asp Pro Gly Gln Arg Gly Arg His			
	260	265	270
His Gln Gly Gly His Asp Pro Gly Arg Gln Gly Ala Gln Arg Gly Thr			

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(2) INFORMATION FOR SEQ ID NO:75:

(A) LENGTH: 580 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Ser	Ala	Val	Trp	Cys	Leu	Asn	Gly	Phe	Thr	Gly	Arg	His	Arg	His	Gly
1				5					10					15	
Arg	Cys	Arg	Val	Arg	Ala	Ser	Gly	Trp	Arg	Ser	Ser	Asn	Arg	Trp	Cys
			20					25					30		
Ser	Thr	Thr	Ala	Asp	Cys	Cys	Ala	Ser	Lys	Thr	Pro	Thr	Gln	Ala	Ala
			35				40					45			
Ser	Pro	Leu	Glu	Arg	Arg	Phe	Thr	Cys	Cys	Ser	Pro	Ala	Val	Gly	Cys
	50					55					60				
Arg	Phe	Arg	Ser	Phe	Pro	Val	Arg	Arg	Leu	Ala	Leu	Gly	Ala	Arg	Thr
65					70					75					80
Ser	Arg	Thr	Leu	Gly	Val	Arg	Arg	Thr	Leu	Ser	Gln	Trp	Asn	Leu	Ser
				85					90					95	
Pro	Arg	Ala	Gln	Pro	Ser	Cys	Ala	Val	Thr	Val	Glu	Ser	His	Thr	His
			100					105					110		
Ala	Ser	Pro	Arg	Met	Ala	Lys	Leu	Ala	Arg	Val	Val	Gly	Leu	Val	Gln
			115				120					125			
Glu	Glu	Gln	Pro	Ser	Asp	Met	Thr	Asn	His	Pro	Arg	Tyr	Ser	Pro	Pro
	130					135					140				
Pro	Gln	Gln	Pro	Gly	Thr	Pro	Gly	Tyr	Ala	Gln	Gly	Gln	Gln	Gln	Thr
145					150					155					160
Tyr	Ser	Gln	Gln	Phe	Asp	Trp	Arg	Tyr	Pro	Pro	Ser	Pro	Pro	Pro	Gln
				165					170					175	
Pro	Thr	Gln	Tyr	Arg	Gln	Pro	Tyr	Glu	Ala	Leu	Gly	Gly	Thr	Arg	Pro
			180					185					190		
Gly	Leu	Ile	Pro	Gly	Val	Ile	Pro	Thr	Met	Thr	Pro	Pro	Pro	Gly	Met
		195					200					205			
Val	Arg	Gln	Arg	Pro	Arg	Ala	Gly	Met	Leu	Ala	Ile	Gly	Ala	Val	Thr
	210					215					220				
Ile	Ala	Val	Val	Ser	Ala	Gly	Ile	Gly	Gly	Ala	Ala	Ala	Ser	Leu	Val
225					230					235					240
Gly	Phe	Asn	Arg	Ala	Pro	Ala	Gly	Pro	Ser	Gly	Gly	Pro	Val	Ala	Ala
				245					250					255	
Ser	Ala	Ala	Pro	Ser	Ile	Pro	Ala	Ala	Asn	Met	Pro	Pro	Gly	Ser	Val
			260					265					270		
Glu	Gln	Val	Ala	Ala	Lys	Val	Val	Pro	Ser	Val	Val	Met	Leu	Glu	Thr
		275					280					285			
Asp	Leu	Gly	Arg	Gln	Ser	Glu	Glu	Gly	Ser	Gly	Ile	Ile	Leu	Ser	Ala
	290					295					300				
Glu	Gly	Leu	Ile	Leu	Thr	Asn	Asn	His	Val	Ile	Ala	Ala	Ala	Ala	Lys

305 310 315 320
 Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp
 325 330 335
 Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp
 340 345 350
 Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser
 355 360 365
 Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile
 370 375 380
 Gly Ser Pro Leu Gly Leu Glu Gly Thr Val Thr Thr Gly Ile Val Ser
 385 390 395 400
 Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Glu Ala Gly Asn Gln Asn
 405 410 415
 Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn
 420 425 430
 Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn
 435 440 445
 Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly
 450 455 460
 Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile
 465 470 475 480
 Ala Asp Glu Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly
 485 490 495
 Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu
 500 505 510
 Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val
 515 520 525
 Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu
 530 535 540
 Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr
 545 550 555 560
 Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly
 565 570 575
 Lys Ala Glu Gln
 580

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
 1 5 10 15
 Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
 20 25 30
 Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
 35 40 45
 Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
 50 55 60
 Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu

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(2) INFORMATION FOR SEQ ID NO:77:

(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Val	Pro	Pro	Ala	Pro	Pro	Leu	Pro	Pro	Leu	Pro	Pro	Ser	Pro	Ile	Ser
1			5						10					15	

Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
 20 25 30
 Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
 35 40 45
 Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
 50 55 60
 Ser Pro Pro Leu Pro
 65

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 1 5 10 15
 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 20 25 30
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285

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Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr
 1 5 10 15
 Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala
 20 25 30
 Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
 35 40 45
 Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
 50 55 60
 Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly
 65 70 75 80
 Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp
 85 90 95
 Asp Trp Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val
 100 105 110
 Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn
 115 120 125
 Leu Gln Ala Gln Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys
 130 135 140
 Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
 145 150 155 160
 Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser
 165 170 175
 His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln
 180 185 190
 Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp
 195 200 205

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1 5 10 15
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
 20 25 30
 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
 35 40 45
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
 50 55 60
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
 65 70 75 80
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
 85 90 95
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
 100 105 110
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
 115 120 125
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
 130 135 140
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
 145 150 155 160
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
 165 170 175
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
 180 185 190
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
 195 200 205
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
 210 215 220
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
 225 230 235 240
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
 245 250 255
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
 260 265 270
 Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
 275 280 285

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr
 1 5 10 15
 Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp
 20 25 30
 Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg

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35	40	45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg		
50	55	60
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro		
65	70	75
Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp		
85	90	95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu		
100	105	110
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val		
115	120	125
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn		
130	135	140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro		
145	150	155
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu		
165	170	

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile	
1	5
Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Gly	
20	25
Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro	
35	40
Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa	
50	55
Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp	
65	70
Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile	
85	90
Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Xaa Gln	
100	105

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn	
1	5
Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr	
10	15

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(2) INFORMATION FOR SEQ ID NO:85:

(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

[illegible]

(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
1 5 10 15
Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
20 25 30

Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
 35 40 45
 Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
 50 55 60
 His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
 65 70 75 80
 Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
 85 90 95
 Pro Ala Ala Gly Gly Gly Ala
 100

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly
 1 5 10 15
 Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His
 20 25 30
 Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala
 35 40 45
 Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly
 50 55 60
 Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly
 65 70 75 80
 Asp Glu Leu Lys Gly Val Thr Ser
 85

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
 1 5 10 15
 Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
 20 25 30
 Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
 35 40 45
 Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
 50 55 60
 Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 65 70 75 80
 Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe

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85

90

95

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
1      5      10      15
Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
20     25     30
Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
35     40     45
Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
50     55     60
Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
65     70     75     80
Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
85     90     95
Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100    105    110
Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115    120    125
Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130    135    140
Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
145    150    155    160
Leu Thr Leu Gln Gly Asp
165

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Arg Ala Glu Arg Met
1      5

```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
 1 5 10 15
 Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
 20 25 30
 Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
 35 40 45
 Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
 50 55 60
 Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
 65 70 75 80
 Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
 85 90 95
 Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
 100 105 110
 Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
 115 120 125
 Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
 130 135 140
 Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
 145 150 155 160
 His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
 165 170 175
 Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
 180 185 190
 Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala
 195 200 205
 Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
 210 215 220
 Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
 225 230 235 240
 Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
 245 250 255
 Arg Arg Asn Gly Gly Pro Ala
 260

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala
 1 5 10 15
 Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly
 20 25 30
 Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly
 35 40 45
 Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr

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50		55		60
Glu	Leu	Gly	Gly	Gly
65		70		75
Val	Gly	Val	Ala	Leu
		85		90
Pro	Lys	Ala	Lys	Ser
		100		105
Gly	Val	Phe	Leu	Met
		115		120
Ser	Thr	Gly	Trp	Ala
		130		135
Ala	Val	Ala	Ala	Val
		145		150
Ala	Pro	Ala	Pro	Arg
		165		170
Tyr	Gly	Gln	Tyr	Gly
		180		185
Gln	Gln	Gly	Ala	Gln
		195		200
Gln	Ser	Pro	Gln	Pro
		210		215
Ser	Ser	Pro	Ser	Gln
		225		230
Gln	Pro	Pro	Ala	Gln
		245		250
Thr	Pro	Pro	Thr	Gly
		260		265
Ala	Gly	Thr	Gly	Ser
		275		280
Pro	Ser	Gly	Gly	Glu
		290		295
				300

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Gly	Cys	Gly	Glu	Thr	Asp	Ala	Ala	Thr	Leu	Ala	Gln	Glu	Ala	Gly	Asn
1				5				10						15	
Phe	Glu	Arg	Ile	Ser	Gly	Asp	Leu	Lys	Thr	Gln	Ile				
			20					25							

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp	Gln	Val	Glu	Ser	Thr	Ala	Gly	Ser	Leu	Gln	Gly	Gln	Trp	Arg	Gly
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Gly	Cys	Gly	Ser	Thr	Ala	Gly	Ser	Leu	Gln	Gly	Gln	Trp	Arg	Gly	Ala
1				5				10						15	
Ala	Gly	Thr	Ala	Ala	Gln	Ala	Ala	Val	Val	Arg					
			20				25								

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Gly	Cys	Gly	Gly	Thr	Ala	Ala	Gln	Ala	Ala	Val	Val	Arg	Phe	Gln	Glu
1				5				10						15	
Ala	Ala	Asn	Lys	Gln	Lys	Gln	Glu	Leu	Asp	Glu					
			20				25								

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Gly	Cys	Gly	Ala	Asn	Lys	Gln	Lys	Gln	Glu	Leu	Asp	Glu	Ile	Ser	Thr
1				5				10						15	
Asn	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg					
			20				25								

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 amino acids

10084843.022502

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly	Cys	Gly	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg	Ala	Asp	Glu
1			5					10					15		
Glu	Gln	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	Phe				
			20					25							

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGAAGATGG	TGAAATCGAT	CGCCGCAGGT	CTGACCGCCG	CGGCTGCAAT	CGGCGCCGCT	60
GCGGCCGGTG	TGACTTCGAT	CATGGCTGGC	GGCCCGGTTCG	TATACCAGAT	GCAGCCGGTC	120
GTCTTCGGCG	CGCCACTGCC	GTTGGACCCG	GCATCCGCCC	CTGACGTCCC	GACCGCCGCC	180
CAGTTGACCA	GCCTGCTCAA	CAGCCTCGCC	GATCCCAACG	TGTCGTTTGC	GAACAAGGGC	240
AGTCTGGTCG	AGGGCGGCAT	CGGGGGCACC	GAGGCGCGCA	TCGCCGACCA	CAAGCTGAAG	300
AAGGCCGCCG	AGCACGGGGA	TCTGCCGCTG	TCGTTTCAGC	TGACGAACAT	CCAGCCGGCG	360
GCCGCCGGTT	CGGCCACCGC	CGACGTTTCC	GTCTCGGGTC	CGAAGCTCTC	GTCGCCGGTC	420
ACGCAGAACG	TCACGTTTCG	GAATCAAGGC	GGCTGGATGC	TGTCACGCGC	ATCGGCGATG	480
GAGTTGCTGC	AGGCCGCAGG	GAAGTGA				507

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met	Lys	Met	Val	Lys	Ser	Ile	Ala	Ala	Gly	Leu	Thr	Ala	Ala	Ala	Ala
1			5						10				15		
Ile	Gly	Ala	Ala	Ala	Ala	Gly	Val	Thr	Ser	Ile	Met	Ala	Gly	Gly	Pro
			20					25				30			
Val	Val	Tyr	Gln	Met	Gln	Pro	Val	Val	Phe	Gly	Ala	Pro	Leu	Pro	Leu
		35				40				45					
Asp	Pro	Ala	Ser	Ala	Pro	Asp	Val	Pro	Thr	Ala	Ala	Gln	Leu	Thr	Ser
	50				55				60						
Leu	Leu	Asn	Ser	Leu	Ala	Asp	Pro	Asn	Val	Ser	Phe	Ala	Asn	Lys	Gly
65			70					75					80		
Ser	Leu	Val	Glu	Gly	Gly	Ile	Gly	Gly	Thr	Glu	Ala	Arg	Ile	Ala	Asp
			85				90					95			
His	Lys	Leu	Lys	Lys	Ala	Ala	Glu	His	Gly	Asp	Leu	Pro	Leu	Ser	Phe

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(2) INFORMATION FOR SEQ ID NO:101:

(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

CGTGGCAATG	TCGTTGACCG	TCGGGGGCCGG	GGTCGCCTCC	GCAGATCCCG	TGGACGCGGT	60
CATTAACACC	ACCTGCAATT	ACGGGCAGGT	AGTAGCTGCG	CTCAACGCGA	CGGATCCGGG	120
GGCTGCCGCA	CAGTTCAACG	CCTCACCGGT	GGCGCAGTCC	TATTTGCGCA	ATTTCCTCGC	180
CGCACCGCCA	CCTCAGCGCG	CTGCCATGGC	CGCGCAATTG	CAAGCTGTGC	CGGGGGCGGC	240
ACAGTACATC	GGCCTTGTCG	AGTCGGTTGC	CGGCTCCTGC	AACAACATT	AAGCCCATGC	300
GGGCCCATC	CCGCGACCCG	GCATCGTCGC	CGGGGCTAGG	CCAGATTGCC	CCGCTCCTCA	360
ACGGGCCGCA	TCCGCGGACC	CGGCATCGTC	GCCGGGGCTA	GGCCAGATTG	CCCCGCTCCT	420
CAACGGGCCG	CATCTCGTGC	CGAATTCTTG	CAGCCCGGGG	GATCCACTAG	TTCTAGAGCG	480
GCCGCCACCG	CGGTGGAGCT					500

(A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Val	Ala	Met	Ser	Leu	Thr	Val	Gly	Ala	Gly	Val	Ala	Ser	Ala	Asp	Pro
1				5					10					15	
Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala
			20					25						30	
Ala	Leu	Asn	Ala	Thr	Asp	Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser
		35					40					45			
Pro	Val	Ala	Gln	Ser	Tyr	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro
	50					55					60				
Gln	Arg	Ala	Ala	Met	Ala	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala
65				70					75						80
Gln	Tyr	Ile	Gly	Leu	Val	Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr
				85					90					95	

(2) INFORMATION FOR SEO ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGCGC AATCCAGGGA      60
AATGTCACGT CCATTCATTC CCTCCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA      120
GCGGCCTGGG GCGGTAGCGG TTCGGAAGCG TACC                                     154

```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
 1             5             10             15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
          20             25             30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
          35             40             45
Glu Ala Tyr
 50

```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

CGGTCGCGCA CTTCCAGGTG ACTATGAAAG TCGGCTTCCG NCTGGAGGAT TCCTGAACCT      60
TCAAGCGCGG CCGATAACTG AGGTGCATCA TTAAGCGACT TTTCCAGAAC ATCCTGACGC      120
GCTCGAAACG CGGCACAGCC GACGGTGGCT CCGNCGAGGC GCTGNCTCCA AAATCCCTGA      180
GACAATTTCG CGGGGGCGCC TACAAGGAAG TCGGTGCTGA ATTCGNCGNG TATCTGGTCG      240
ACCTGTGTGG TCTGNAGCCG GACGAAGCGG TGCTCGACGT CG                                     282

```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC	GTGCGAGTGC	TCGGGCCGTT	TGAGGATGGA	GTGCACGTGT	CTTTCGTGAT	60
GGCATACCCA	GAGATGTTGG	CGGCGGCGGC	TGACACCCTG	CAGAGCATCG	GTGCTACCAC	120
TGTGGCTAGC	AATGCCGCTG	CGGCGGCCCC	GACGACTGGG	GTGGTGCCCC	CCGCTGCCGA	180
TGAGGTGTCG	GCGCTGACTG	CGGCGCACTT	CGCCGCACAT	GCGGCGATGT	ATCAGTCCGT	240
GAGCGCTCGG	GCTGCTGCGA	TTCATGACCA	GTTCGTGGCC	ACCCTTGCCA	GCAGCGCCAG	300
CTCGTATGCG	GCCACTGAAG	TCGCCAATGC	GGCGGCGGCC	AGCTAAGCCA	GGAACAGTCG	360
GCACGAGAAA	CCACGAGAAA	TAGGGACACG	TAATGGTGGA	TTTCGGGGCG	TTACCACCGG	420
AGATCAACTC	CGCGAGGATG	TACGCCGGCC	CGGGTTCGGC	CTCGCTGGTG	GCCGCGGCTC	480
AGATGTGGGA	CAGCGTGGCG	AGTGACCTGT	TTTCGGCCGC	GTCGGCGTTT	CAGTCGGTGG	540
TCTGGGGTCT	GACGGTGGGG	TCGTGGATAG	GTTCGTGGC	GGGTCTGATG	GTGGCGGCGG	600
CCTCGCCGTA	TGTGGCGTGG	ATGAGCGTCA	CCGCGGGGCA	GGCCGAGCTG	ACCGCCGCCC	660
AGGTCCGGGT	TGCTGCGGCG	GCCTACGAGA	CGGCGTATGG	GCTGACGGTG	CCCCCGCCGG	720
TGATCGCCGA	GAACCGTGCT	GAAGTATGA	TTCTGATAGC	GACCAACCTC	TTGGGGCAAA	780
ACACCCCGGC	GATCGCGGTC	AACGAGGCCG	AATACGGCGA	GATGTGGGCC	CAAGACGCCG	840
CCGCGATGTT	TGGCTACGCC	GCGGCGACGG	CGACGGCGAC	GGCGACGTTG	CTGCCGTTTCG	900
AGGAGGCGCC	GGAGATGACC	AGCGCGGGTG	GGCTCCTCGA	GCAGGCCGCC	GCGGTCGAGG	960
AGGCCTCCGA	CACCGCCGCG	GCGAACCAGT	TGATGAACAA	TGTGCCCCAG	GCGCTGCAAC	1020
AGCTGGCCCA	GCCCACGCAG	GGCACCACGC	CTTCTTCCAA	GCTGGGTGGC	CTGTGGAAGA	1080
CGGTCTCGCC	GCATCGGTCTG	CCGATCAGCA	ACATGGTGTC	GATGGCCAAC	AACCACATGT	1140
CGATGACCAA	CTCGGGTGTG	TCGATGACCA	ACACCTTGAG	CTCGATGTTG	AAGGGCTTTG	1200
CTCCGGCGGC	GGCCGCCCAG	GCCGTGCAAA	CCGCGGCGCA	AAACGGGGTC	CGGGCGATGA	1260
GCTCGCTGGG	CAGCTCGCTG	GGTTCTTCGG	GTCTGGGCGG	TGGGGTGGCC	GCCAACTTGG	1320
GTCGGGCGGC	CTCGGTCGGT	TCGTTGTCGG	TGCCGCAGGC	CTGGGCCGCG	GCCAACCAGG	1380
CAGTCACCCC	GGCGGCGCGG	GCGCTGCCGC	TGACCAGCCT	GACCAGCGCC	GCGGAAAGAG	1440
GGCCCGGGCA	GATGCTGGGC	GGGCTGCCGG	TGGGGCAGAT	GGGCGCCAGG	GCCGGTGGTG	1500
GGCTCAGTGG	TGTGCTGCGT	GTTCCGCCGC	GACCCTATGT	GATGCCGCAT	TCTCCGGCGG	1560
CCGGCTAGGA	GAGGGGGCGC	AGACTGTCGT	TATTTGACCA	GTGATCGGCG	GTCTCGGTGT	1620

TTCCGCGGCC GGCTATGACA ACAGTCAATG TGCATGACAA GTTACAGGTA TTAGGTCCAG 1680
 GTTCAACAAG GAGACAGGCA ACATGGCCTC ACGTTTATG ACGGATCCGC ACGCGATGCG 1740
 GGACATGGCG GGCCGTTTTG AGGTGCACGC CCAGACGGTG GAGGACGAGG CTCGCCGGAT 1800
 GTGGGCGTCC GCGCAAAACA TTTCCGGTGC GGGCTGGAGT GGCATGGCCG AGGCGACCTC 1860
 GCTAGACACC ATGGCCCAGA TGAATCAGGC GTTTCGCAAC ATCGTGAACA TGCTGCACGG 1920
 GGTGCGTGAC GGGCTGGTTC GCGACGCCAA CAACTACGAG CAGCAAGAGC AGGCCTCCCA 1980
 GCAGATCCTC AGCAGCTAAC GTCAGCCGCT GCAGCACAAT ACTTTTACAA GCGAAGGAGA 2040
 ACAGGTTCCA TGACCATCAA CTATCAATTC GGGGATGTCT ACGCTCACGG CGCCATGATC 2100
 CGCGCTCAGG CCGGGTTGCT GGAGGCCGAG CATCAGGCCA TCATTCTGTA TGTGTTGACC 2160
 GCGAGTGAAT TTTGGGGCGG CGCCGGTTCG GCGGCCTGCC AGGGGTTCAT TACCCAGTTG 2220
 GGCCGTAAC TCCAGGTGAT CTACGAGCAG GCCAACGCCC ACGGGCAGAA GGTGCAGGCT 2280
 GCCGGCAACA ACATGGCGCA AACCGACAGC GCCGTCGGCT CCAGCTGGGC CTGACACCAG 2340
 GCCAAGGCCA GGGACGTGGT GTACGAGTGA AGTTCCTCGC GTGATCCTTC GGGTGGCAGT 2400
 CTAAGTGGTC AGTGCTGGGG TGTGTTGGT TTGCTGCTTG GCGGGTTCTT CGGTGCTGGT 2460
 CAGTGCTGCT CGGGCTCGGG TGAGGACCTC GAGGCCCAGG TAGCGCCGTC CTTGATCCA 2520
 TTCGTCGTGT TGTTCGGCGA GGACGGCTCC GACGAGGCGG ATGATCGAGG CGCGGTCGGG 2580
 GAAGATGCCC ACGACGTCGG TTCGGCGTCG TACCTCTCGG TTGAGGCGTT CCTGGGGGTT 2640
 GTTGGACCAG ATTTGGCGCC AGATCTGCTT GGGGAAGGCG GTGAACGCCA GCAGGTCGGT 2700
 GCGGGCGGTG TCGAGGTGCT CGGCCACCGC GGGGAGTTTG TCGGTCAGAG CGTCGAGTAC 2760
 CCGATCATAT TGGGCAACAA CTGATTCGGC GTCGGGCTGG TCGTAGATGG AGTGCAGCAG 2820
 GGTGCGCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG 2880
 GGTCTGTCAG CGCTGCCAGG CCGCTGCGGG CAGGGTGGCG CCGATCGCGG CCACCAGGCC 2940
 GGCCTGGGCG TCGCTGGTGA CCAGCGCGAC CCCGGACAGG CCGCGGGCGA CCAGGTCGCG 3000
 GAAGAACGCC AGCCAGCCGG CCCCCTCCTC GGCGGAGGTG ACCTGGATGC CCAGGATC 3058

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

10084843.022502

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met	Val	Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	1	5	10	15
Tyr	Ala	Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp	20	25	30	
Asp	Ser	Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	35	40	45	
Val	Val	Trp	Gly	Leu	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	50	55	60	
Leu	Met	Val	Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	65	70	75	80
Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	85	90	95	
Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	100	105	110	
Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	115	120	125	
Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	130	135	140	
Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	145	150	155	160
Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	165	170	175	
Ser	Ala	Gly	Gly	Leu	Leu	Glu	Gln	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	180	185	190	
Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	195	200	205	
Gln	Gln	Leu	Ala	Gln	Pro	Thr	Gln	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	210	215	220	
Gly	Gly	Leu	Trp	Lys	Thr	Val	Ser	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	225	230	235	240
Met	Val	Ser	Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	245	250	255	
Ser	Met	Thr	Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	260	265	270	

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Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285

Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320

Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380

Pro His Ser Pro Ala Ala Gly
 385 390

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GACGTCAGCA CCCGCCGTGC AGGGCTGGAG CGTGGTCGGT TTTGATCTGC GGTCAAGGTG	60
ACGTCCCTCG GCGTGTGCGC GCGGTGGATG CAGACTCGAT GCCGCTCTTT AGTGCAACTA	120
ATTTGTTGA AGTGCCTGCG AGGTATAGGA CTTACAGATT GGTTAATGTA GCGTTCACCC	180
CGTGTTGGGG TCGATTGGC CGGACCAGTC GTCACCAACG CTTGGCGTGC GCGCCAGGCG	240
GGCGATCAGA TCGCTTGA CTCAATCAAT CTTGAGCTCC CGGGCCGATG CTCGGGCTAA	300
ATGAGGAGGA GCACGCGTGT CTTTCACTGC GCAACCGGAG ATGTTGGCGG CCGCGGCTGG	360
CGAACTTCGT TCCCTGGGGG CAACGCTGAA GGCTAGCAAT GCCGCCGCAG CCGTGCCGAC	420
GA CTGGGGTG GTGCCCCCGG CTGCCGACGA GGTGTCGCTG CTGCTTGCCA CACAATTCCG	480
TACGCATGCG GCGACGTATC AGACGGCCAG CGCCAAGGCC GCGGTGATCC ATGAGCAGTT	540
TGTGACCACG CTGGCCACCA GCGCTAGTTC ATATGCGGAC ACCGAGGCCG CCAACGCTGT	600
GGTCACCGGC TAGCTGACCT GACGGTATTC GAGCGGAAGG ATTATCGAAG TGGTGGATTT	660

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CGGGGCGTTA CCACCGGAGA TCAACTCCGC GAGGATGTAC GCCGGCCCCG GTTCGGCCTC 720
GCTGGTGGCC GCCGCGAAGA TGTGGGACAG CGTGGCGAGT GACCTGTTTT CGGCCGCGTC 780
GGCGTTTCAG TCGGTGGTCT GGGGTCTGAC GGTGGGGTCG TGGATAGGT^T CGTCGGCGGG 840
TCTGATGGCG GCGGCGGCCT CGCCGTATGT GCGGTGGATG AGCGTCACCG CGGGGCAGGC 900
CCAGCTGACC GCCGCCCAGG TCCGGGTTGC TCGGGCGGCC TACGAGACAG CGTATAGGCT 960
GACGGTGCCC CCGCCGGTGA TCGCCGAGAA CCGTACCGAA CTGATGACGC TGACCGCGAC 1020
CAACCTCTTG GGGCAAAACA CGCCGGCGAT CGAGGCCAAT CAGGCCGCAT ACAGCCAGAT 1080
GTGGGGCCAA GACGCGGAGG ~~CGATGTATGG~~ ~~CTACGCCGCC~~ ACGGCGGCGA CGGCGACCGA 1140
GGCGTTGCTG CCGTTCGAGG ACGCCCCACT GATCACCAAC CCCGGCGGGC TCCTTGAGCA 1200
GGCCGTGCGG GTCGAGGAGG CCATCGACAC CGCCGCGGCG AACCAGTTGA TGAACAATGT 1260
GCCCCAAGCG CTGCAACAGC TGGCCCAGCC AGCGCAGGGC GTCGTACCTT CTTCCAAGCT 1320
GGGTGGGCTG TGGACGGCGG TCTCGCCGCA TCTGTCGCCG CTCAGCAACG TCAGTTCGAT 1380
AGCCAACAAC CACATGTCGA TGATGGGCAC GGGTGTGTCG ATGACCAACA CCTTGCACTC 1440
GATGTTGAAG GGCTTAGCTC CGGCGGCGGC TCAGGCCGTG GAAACCGCGG CGGAAAACGG 1500
GGTCTGGGCG ATGAGCTCGC TGGGCAGCCA GCTGGGTTCT TCGCTGGGTT CTTGGGTCT 1560
GGGCGCTGGG GTGGCCGCCA ACTTGGGTCT GCGGCCTCTG GTCGGTTCGT TGTCGGTGCC 1620
GCCAGCATGG GCCGCGGCCA ACCAGGCGGT CACCCCGGCG GCGCGGGCGC TGCCGCTGAC 1680
CAGCCTGACC AGCGCCGCC AAACCGCCCC CGGACACATG CTGGG 1725

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
1 5 10 15
Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
20 25 30
Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
35 40 45

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Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Thr Glu Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met
 130 135 140
 Trp Gly Gln Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
 145 150 155 160
 Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
 165 170 175
 Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn
 225 230 235 240
 Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala
 260 265 270
 Ala Ala Gln Ala Val Glu Thr Ala Ala Glu Asn Gly Val Trp Ala Met
 275 280 285
 Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu
 290 295 300
 Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
 305 310 315 320
 Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro
 325 330 335

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Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
 340 345 350

Ala Pro Gly His Met Leu Gly
 355

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3027 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGTTCAGTCG AGAATGATAC TGACGGGCTG TATCCACGAT GGCTGAGACA ACCGAACCAC	60
CGTCGGACGC GGGGACATCG CAAGCCGACG CGATGGCGTT GGCCGCCGAA GCCGAAGCCG	120
CCGAAGCCGA AGCGCTGGCC GCCGCGGCGC GGGCCCGTGC CCGTGCCGCC CGGTTGAAGC	180
GTGAGGCGCT GGCATGGCC CCAGCCGAGG ACGAGAACGT CCCCAGGAT ATGCAGACTG	240
GGAAGACGCC GAAGACTATG ACGACTATGA CGACTATGAG GCCGCAGACC AGGAGGCCGC	300
ACGGTCGGCA TCCTGGCGAC GGCAGTTGCG GGTGCGGTTA CCAAGACTGT CCACGATTGC	360
CATGGCGGCC GCAGTCGTCA TCATCTGCGG CTTACCGGG CTCAGCGGAT ACATTGTGTG	420
GCAACACCAT GAGGCCACCG AACGCCAGCA GCGCGCCGCG GCGTTCGCCG CCGGAGCCAA	480
GCAAGGTGTC ATCAACATGA CCTCGCTGGA CTTCAACAAG GCCAAAGAAG ACGTCGCGCG	540
TGTGATCGAC AGCTCCACCG GCGAATTCAG GGATGACTTC CAGCAGCGGG CAGCCGATTT	600
CACCAAGGTT GTCGAACAGT CCAAAGTGGT CACCGAAGGC ACGGTGAACG CGACAGCCGT	660
CGAATCCATG AACGAGCATT CCGCCGTGGT GCTCGTCGCG GCGACTTCAC GGGTCACCAA	720
TTCCGCTGGG GCGAAAGACG AACCACGTGC GTGGCGGCTC AAAGTGACCG TGACCGAAGA	780
GGGGGGACAG TACAAGATGT CGAAAGTTGA GTTCGTACCG TGACCGATGA CGTACGCGAC	840
GTCAACACCG AAACCACTGA CGCCACCGAA GTCGCTGAGA TCGACTCAGC CGCAGGCGAA	900
GCCGGTGATT CGGCGACCGA GGCATTTGAC ACCGACTCTG CAACGGAATC TACCGCGCAG	960
AAGGGTCAGC GGCACCGTGA CCTGTGGCGA ATGCAGGTTA CCTTGAAACC CGTTCCGGTG	1020
ATTCTCATCC TGCTCATGTT GATCTCTGGG GGC GCGACGG GATGGCTATA CCTTGAGCAA	1080
TACGACCCGA TCAGCAGACG GACTCCGGCG CCGCCCGTGC TGCCGTCGCC GCGGCGTCTG	1140
ACGGGACAAT CGCGCTGTTG TGTATTCACC CGACACGTCG ACCAAGACTT CGCTACCGCC	1200

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AGGTCGCACC	TCGCCGGCGA	TTTCCTGTCC	TATACGACCA	GTTACGCAG	CAGATCGTGG	1260
CTCCGGCGGC	CAAACAGAAG	TCACTGAAAA	CCACCGCCAA	GGTGGTGCGC	GCGGCCGTGT	1320
CGGAGCTACA	TCCGGATTCT	GCCGTCGTTC	TGGTTTTTGT	CGACCAGAGC	ACTACCAGTA	1380
AGGACAGCCC	CAATCCGTCG	ATGGCGGCCA	GCAGCGTGAT	GGTGACCCTA	GCCAAGGTCG	1440
ACGGCAATTG	GCTGATCACC	AAGTTCACCC	CGGTTTAGGT	TGCCGTAGGC	GGTCGCCAAG	1500
TCTGACGGGG	GCGCGGGTGG	CTGCTCGTGC	GAGATACCGG	CCGTTCTCCG	GACAATCACG	1560
GCCCCGACCTC	AAACAGATCT	CGGCCGCTGT	CTAATCGGCC	GGGTTATTTA	AGATTAGTTG	1620
CCACTGTATT	TACCTGATGT	TCAGATTGTT	CAGCTGGATT	TAGCTTCGCG	GCAGGGCGGC	1680
TGGTGCACTT	TGCATCTGGG	GTTGTGACTA	CTTGAGAGAA	TTTGACCTGT	TGCCGACGTT	1740
GTTTGCTGTC	CATCATTGGT	GCTAGTTATG	GCCGAGCGGA	AGGATTATCG	AAGTGGTGGA	1800
CTTCGGGGCG	TTACCACCGG	AGATCAACTC	CGCGAGGATG	TACGCCGGCC	CGGGTTCGGC	1860
CTCGCTGGTG	GCCGCCGCGA	AGATGTGGGA	CAGCGTGCGC	AGTGACCTGT	TTTCGGCCGC	1920
GTCGGCGTTT	CAGTCGGTGG	TCTGGGGTCT	GACGACGGGA	TCGTGGATAG	GTTCGTCGGC	1980
GGGTCTGATG	GTGGCGGCGG	CCTCGCCGTA	TGTGGCGTGG	ATGAGCGTCA	CCGCGGGGCA	2040
GGCCGAGCTG	ACCGCCGCCC	AGGTCCGGGT	TGCTGCGGCG	GCCTACGAGA	CGGCGTATGG	2100
GCTGACGGTG	CCCCCGCCGG	TGATCGCCGA	GAACCGTGCT	GAAGTGATGA	TTCTGATAGC	2160
GACCAACCTC	TTGGGGCAAA	ACACCCCGGC	GATCGCGGTC	AACGAGGCCG	AATACGGGGA	2220
GATGTGGGCC	CAAGACGCCG	CCGCGATGTT	TGGCTACGCC	GCCACGGCGG	CGACGGCGAC	2280
CGAGGCGTTG	CTGCCGTTCT	AGGACGCCCC	ACTGATCACC	AACCCCGGCG	GGCTCCTTGA	2340
GCAGGCCGTC	GCGGTCGAGG	AGGCCATCGA	CACCGCCGCG	GCGAACCAGT	TGATGAACAA	2400
TGTGCCCCAA	GCGCTGCAAC	AACTGGCCCA	GCCCACGAAA	AGCATCTGGC	CGTTCGACCA	2460
ACTGAGTGAA	CTCTGGAAAG	CCATCTCGCC	GCATCTGTCT	CCGCTCAGCA	ACATCGTGTC	2520
GATGCTCAAC	AACCACGTGT	CGATGACCAA	CTCGGGTGTG	TCGATGGCCA	GCACCTTGCA	2580
CTCAATGTTG	AAGGGCTTTG	CTCCGGCGGC	GGCTCAGGCC	GTGGAAACCG	CGGCGCAAAA	2640
CGGGGTCCAG	GCGATGAGCT	CGCTGGGCAG	CCAGCTGGGT	TCGTGCTGG	GTTCTTCGGG	2700
TCTGGGCGCT	GGGGTGGCCG	CCAACCTGGG	TCGGGCGGCC	TCGGTTCGGT	CGTTGTGCGT	2760
GCCGCAGGCC	TGGGCCGCGG	CCAACCAGGC	GGTCACCCCG	GCGGCGCGGG	CGCTGCCGCT	2820

GACCAGCCTG ACCAGCGCCG CCCAAACCGC CCCC GGACAC ATGCTGGGCG GGCTACCGCT 2880
 GGGGCAACTG ACCAATAGCG GCGGCGGGTT CGGCGGGGTT AGCAATGCGT TCGGGATGCC 2940
 GCCGCGGGCG TACGTAATGC CCCGTGTGCC CGCCGCCGGG TAACGCCGAT CCGCACGCAA 3000
 TCGGGGCCCT CTATGCGGGC AGCGATC 3027

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Val	Val	Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	1	5	10	15
Tyr	Ala	Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Lys	Met	Trp	20	25	30	
Asp	Ser	Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	35	40	45	
Val	Val	Trp	Gly	Leu	Thr	Thr	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	50	55	60	
Leu	Met	Val	Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	65	70	75	80
Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	85	90	95	
Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	100	105	110	
Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	115	120	125	
Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	130	135	140	
Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Thr	Ala	Ala	145	150	155	160
Thr	Ala	Thr	Glu	Ala	Leu	Leu	Pro	Phe	Glu	Asp	Ala	Pro	Leu	Ile	Thr	165	170	175	
Asn	Pro	Gly	Gly	Leu	Leu	Glu	Gln	Ala	Val	Ala	Val	Glu	Glu	Ala	Ile	180	185	190	
Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu				

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195	200	205
Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu 210 215 220		
Ser Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn 225 230 235 240		
Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val 245 250 255		
Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala 260 265 270		
Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met 275 280 285		
Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu 290 295 300		
Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser 305 310 315 320		
Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro 325 330 335		
Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr 340 345 350		
Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn 355 360 365		
Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro 370 375 380		
Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly 385 390 395		

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGGAGGG AGTGATCACC ATGCTGTGGC ACGCAATGCC ACCGGAGTAA ATACCGCACG	60
GCTGATGGCC GGC GCGGGTC CGGCTCCAAT GCTTGCGGCG GCCGCGGGAT GGCAGACGCT	120
TTCGGCGGCT CTGGACGCTC AGGCCGTCGA GTTGACCGCG CGCCTGAACT CTCTGGGAGA	180
AGCCTGGACT GGAGGTGGCA GCGACAAGGC GCTTGCGGCT GCAACGCCGA TGGTGGTCTG	240

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GCTACAAACC GCGTCAACAC AGGCCAAGAC CCGTGCGATG CAGGCGACGG CGCAAGCCGC 300
 GGCATACACC CAGGCCATGG CCACGACGCC GTCGCTGCCG GAGATCGCCG CCAACCACAT 360
 CACCCAGGCC GTCCTTACGG CCACCAACTT CTTCGGTATC AACACGATCC CGATCGCGTT 420
 GACCGAGATG GATTATTTCA TCCGTATGTG GAACCAGGCA GCCCTGGCAA TGGAGGTCTA 480
 CCAGGCCGAG ACCGCGGTTA ACACGCTTTT CGAGAAGCTC GAGCCGATGG CGTCGATCCT 540
 TGATCCCGGC GCGAGCCAGA GCACGACGAA CCCGATCTTC GGAATGCCCT CCCCTGGCAG 600
 CTCAACACCG GTTGGCCAGT TGCCGCCGGC GGCTACCCAG ACCCTCGGCC AACTGGGTGA 660
 GATGAGCGGC CCGATGCAGC AGCTGACCCA GCCGCTGCAG CAGGTGACGT CGTTGTTTCA 720
 CCAGGTGGGC GGCACCGGCG GCGGCAACCC AGCCGACGAG GAAGCCGCGC AGATGGGCCT 780
 GCTCGGCACC AGTCCGCTGT CGAACCATCC GCTGGCTGGT GGATCAGGCC CCAGCGCGGG 840
 CGCGGGCCTG CTGCGCGCGG AGTCGCTACC TGGCGCAGGT GGGTCGTTGA CCCGCACGCC 900
 GCTGATGTCT CAGCTGATCG AAAAGCCGGT TGCCCCCTCG GTGATGCCGG CGGCTGCTGC 960
 CGGATCGTCG GCGACGGGTG GCGCCGCTCC GGTGGGTGCG GGAGCGATGG GCCAGGGTGC 1020
 GCAATCCGGC GGCTCCACCA GGCCGGGTCT GGTCGCGCCG GCACCGCTCG CGCAGGAGCG 1080
 TGAAGAAGAC GACGAGGACG ACTGGGACGA AGAGGACGAC TGGTGAGCTC CCGTAATGAC 1140
 AACAGACTTC CCGGCCACCC GGGCCGGAAG ACTTGCCAAC ATTTTGGCGA GGAAGGTAAA 1200
 GAGAGAAAGT AGTCCAGCAT GGCAGAGATG AAGACCGATG CCGCTACCCT CGCGCAGGAG 1260
 GCAGGTAATT TCGAGCGGAT CTCCGGCGAC CTGAAAACCC AGATCGACCA GGTGGAGTCG 1320
 ACGGCAGGTT CGTTGCAGGG CCAGTGGCGC GGCGCGGCGG GGACGGCCGC CCAGGCCGCG 1380
 GTGGTGCGCT TCCAAGAAGC AGCCAATAAG CAGAAGCAGG AACTCGACGA GATCTCGACG 1440
 AATATTCGTC AGGCCGGCGT CCAATACTCG AGGGCCGACG AGGAGCAGCA GCAGGCGCTG 1500
 TCCTCGCAAA TGGGCTTCTG ACCCGCTAAT ACGAAAAGAA ACGGAGCAAA AACATGACAG 1560
 AGCAGCAGTG GAATTTGCGG GGTATCGAGG CCGCGGCAAG CGCAATCCAG GGAAAT 1616

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

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CTAGTGGATG GGACCATGGC CATTTTCTGC AGTCTCACTG CCTTCTGTGT TGACATTTTG      60
GCACGCCGGC GGAAACGAAG CACTGGGGTC GAAGAACGGC TCGCTGCCA TATCGTCCGG      120
AGCTTCCATA CCTTCGTGCG GCCGGAAGAG CTTGTCTGTAG TCGGCCGCCA TGACAACCTC      180
TCAGAGTGCG CTCAAACGTA TAAACACGAG AAAGGGCGAG ACCGACGGAA GGTCGAACTC      240
GCCCCGATCCC GTGTTTCGCT ATTCTACGCG AACTCGGCGT TGCCCTATGC GAACATCCCA      300
GTGACGTTGC CTTGCGTCGA AGCCATTGCC TGACCGGCTT CGCTGATCGT CCGCGCCAGG      360
TTCTGCAGCG CGTTGTTTCTAG CTCGGTAGCC GTGGCGTCCC ATTTTGTGCTG GACACCCTGG      420
TACGCCTCCG AA                                                                432

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(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```

Met Leu Trp His Ala Met Pro Pro Glu Xaa Asn Thr Ala Arg Leu Met
1           5           10           15
Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala Gly Trp Gln
20           25           30
Thr Leu Ser Ala Ala Leu Asp Ala Gln Ala Val Glu Leu Thr Ala Arg
35           40           45
Leu Asn Ser Leu Gly Glu Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala
50           55           60
Leu Ala Ala Ala Thr Pro Met Val Val Trp Leu Gln Thr Ala Ser Thr
65           70           75           80
Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Ala Tyr
85           90           95
Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Glu Ile Ala Ala Asn
100          105          110
His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn
115          120          125
Thr Ile Pro Ile Ala Leu Thr Glu Met Asp Tyr Phe Ile Arg Met Trp
130          135          140

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Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Glu Thr Ala Val
 145 150 155 160
 Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro
 165 170 175
 Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro
 180 185 190
 Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr
 195 200 205
 Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln
 210 215 220
 Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly
 225 230 235 240
 Gly Gly Asn Pro Ala Asp Glu Glu Ala Ala Gln Met Gly Leu Leu Gly
 245 250 255
 Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser
 260 265 270
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
 275 280 285
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
 290 295 300
 Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly
 305 310 315 320
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
 325 330 335
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
 340 345 350
 Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp
 355 360 365

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
 1 5 10 15

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Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
 20 25 30
 Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
 35 40 45
 Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
 50 55 60
 Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
 65 70 75 80
 Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser
 85 90 95
 Gln Met Gly Phe
 100

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GATCTCCGGC GACCTGAAAA CCCAGATCGA CCAGGTGGAG TCGACGGCAG GTTCGTTGCA	60
GGGCCAGTGG CGCGGCGCGG CGGGGACGGC CGCCCAGGCC GCGGTGGTGC GCTTCCAAGA	120
AGCAGCCAAT AAGCAGAAGC AGGAACTCGA CGAGATCTCG ACGAATATTC GTCAGGCCGG	180
CGTCCAATAC TCGAGGGCCG ACGAGGAGCA GCAGCAGGCG CTGTCCTCGC AAATGGGCTT	240
CTGACCCGCT AATACGAAAA GAAACGGAGC AAAACATGA CAGAGCAGCA GTGGAATTTT	300
GCGGGTATCG AGGCCGCGGC AAGCGCAATC CAGGGAAATG TCACGTCCAT TCATTCCCTC	360
CTTGACGAGG GGAAGCAGTC CCTGACCAAG CTCGCA	396

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala
1 5 10 15

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Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln
 20 25 30
 Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu
 35 40 45
 Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser
 50 55 60
 Arg Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GTGGATCCCG ATCCCGTGTT TCGCTATTCT ACGCGAACTC GGC GTTGCCC TATGCGAACA 60
 TCCCAGTGAC GTTGCCCTTCG GTCGAAGCCA TTGCCTGACC GGCTTCGCTG ATCGTCCGCG 120
 CCAGGTTCTG CAGCGCGTTG TTCAGCTCGG TAGCCGTGGC GTCCCATTTT TGCTGGACAC 180
 CCTGGTACGC CTCCGAACCG CTACCGCCCC AGGCCGCTGC GAGCTTGGTC AGGGACTGCT 240
 TCCCCTCGTC AAGGAGGGAA TGAATGGACG TGACATTTCC CTGGATTGCG CTTGCCGCGG 300
 CCTCGATACC CGCGAAATTC CACTGCTGCT CTGTCATGTT TTTGCTCCGT TTCTTTTCGT 360
 ATTAGCGGGT CAGAAGCCCA TTTGCGA 387

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGCACGAGG ATCTCGGTTG GCCCAACGGC GCTGGCGAGG GCTCCGTTCC GGGGGCGAGC 60
 TGCGCGCCGG ATGCTTCCTC TGCCCGCAGC CGCGCCTGGA TGGATGGACC AGTTGCTACC 120
 TTCCCGACGT TTCGTTCCGGT GTCTGTGCGA TAGCGGTGAC CCCGGCGCGC ACCTCGGGAG 180
 TGTTGGGGGG CAGGCCGGGT CGGTGGTTTC GCCGGGGACG CAGACGGTCT GGACGGAACG 240

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GGCGGGGGTT CGCCGATTGG CATCTTTGCC CA

272

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asp	Pro	Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val
1				5					10					15	
Val Ala Ala Leu															
20															

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1				5					10					15	
Glu Gly Arg															

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr	Tyr	Trp	Cys	Pro	Gly	Gln	Pro	Phe	Asp	Pro	Ala	Trp	Gly	Pro
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp	Ile	Gly	Ser	Glu	Ser	Thr	Glu	Asp	Gln	Gln	Xaa	Ala	Val
1				5				10					

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala	Glu	Glu	Ser	Ile	Ser	Thr	Xaa	Glu	Xaa	Ile	Val	Pro
1				5				10				

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp	Pro	Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro
1				5				10					15		

Ser

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
1 5 10 15
Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn
20 25 30

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp Pro Pro Asp Pro His Gln Xaa Asp Met Thr Lys Gly Tyr Tyr Pro
1 5 10 15
Gly Gly Arg Arg Xaa Phe
20

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Pro Gly Tyr Thr Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Xaa	Xaa	Gly	Phe	Thr	Gly	Pro	Gln	Phe	Tyr
1				5					10

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa	Pro	Xaa	Val	Thr	Ala	Tyr	Ala	Gly
1			5					

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Xaa	Xaa	Xaa	Glu	Lys	Pro	Phe	Leu	Arg
1			5					

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Xaa	Asp	Ser	Glu	Lys	Ser	Ala	Thr	Ile	Lys	Val	Thr	Asp	Ala	Ser
1				5					10				15	

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(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ala Gly Asp Thr Xaa Ile Tyr Ile Val Gly Asn Leu Thr Ala Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ala Pro Glu Ser Gly Ala Gly Leu Gly Gly Thr Val Gln Ala Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Xaa Tyr Ile Ala Tyr Xaa Thr Thr Ala Gly Ile Val Pro Gly Lys Ile
 1 5 10 15

Asn Val His Leu Val
 20

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 882 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

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GCAACGCTGT CGTGGCCTTT GCGGTGATCG GTTTCGCCTC GCTGGCGGTG GCGGTGGCGG 60
 TCACCATCCG ACCGACCGCG GCCTCAAAAC CGGTAGAGGG ACACCAAAAC GCCCAGCCAG 120
 GGAAGTTCAT GCCGTTGTTG CCGACGCAAC AGCAGGCGCC GGTCCCGCCG CCTCCGCCCCG 180
 ATGATCCAC CGCTGGATTC CAGGGCGGCA CCATTCCGGC TGTACAGAAC GTGGTGCCGC 240
 GGCCGGGTAC CTCACCCGGG GTGGGTGGGA CGCCGGCTTC GCCTGCGCCG GAAGCGCCGG 300
 CCGTGCCCGG TGTGTGCCT GCCCCGGTGC CAATCCCGGT CCGATCATC ATTCCCCCGT 360
 TCCCGGGTTG GCAGCCTGGA ATGCCGACCA TCCCCACCGC ACCGCCGACG ACGCCGGTGA 420
 CCACGTGGC GACGACGCCG CCGACCACGC CGCCGACCAC GCCGGTGACC ACGCCGCCAA 480
 CGACGCCGCC GACCACGCCG GTGACCACGC CGCCAACGAC GCCGCCGACC ACGCCGGTGA 540
 CCACGCCACC AACGACCGTC GCCCCGACGA CCGTCGCCCC GACGACGGTC GTCGCCACCA 600
 CCGTCGCCCC GACCACGGTC GTCAGCCA CCGCCACGCC GACGACCGTC GTCGCCAGC 660
 CGACGCAGCA GCCCAGCAA CAACCAACCC AACAGATGCC AACCCAGCAG CAGACCGTGG 720
 CCCCAGAC GGTGGCGCCG GTCGCCAGC CGCCGTCCGG TGGCCGCAAC GGCAGCGGCG 780
 GGGGCGACTT ATTCGGCGGG TTCTGATCAC GGTCGCGGCT TCACTACGGT CGGAGGACAT 840
 GGCCGGTGAT GCGGTGACGG TGGTGCTGCC CTGTCTCAAC GA 882

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CCATCAACCA ACCGCTCGCG CCGCCCGCGC CGCCGGATCC GCCGTCGCCG CCACGCCCCG 60
 CGGTGCCTCC GGTGCCCCCG TTGCCCGCGT CGCCGCCGTC GCCGCCGACC GGCTGGGTGC 120
 CTAGGGCGCT GTTACCGCCC TGGTTGGCGG GGACGCCGCC GGCACCACCG GTACCGCCGA 180
 TGGCGCCGTT GCCGCCGGCG GCACCGTTGC CACCGTTGCC ACCGTTGCCA CCGTTGCCGA 240
 CCAGCCACCC GCCGCGACCA CCGGCACCGC CGGCGCCGCC CGCACCGCCG GCGTGCCCGT 300
 TCGTGCCCGT ACCGCCGGCA CCGCCGTTGC CGCCGTCACC GCCGACGGAA CTACCGGCGG 360
 ACGCGGCCTG CCCGCCGGCG CCGCCCGCAC CGCCATTGGC ACCGCCGTCA CCGCCGGCTG 420

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GGAGTGCCGC GATTAGGGCA CTGACCGGCG CAACCAGCGC AAGTACTCTC GGTCACCGAG 480
 CACTTCCAGA CGACACCACA GCACGGGGTT GTCGGCGGAC TGGGTGAAAT GGCAGCCGAT 540
 AGCGGCTAGC TGTCGGCTGC GGTCAACCTC GATCATGATG TCGAGGTGAC CGTGACCGCG 600
 CCCCCGAAG GAGGCGCTGA ACTCGGCGTT GAGCCGATCG GCGATCGGTT GGGGCAGTGC 660
 CCAGGCCAAT ACGGGGATAC CGGGTGTGNA AGCCGCCGCG AGCGCAGCTT CGGTTGCGCG 720
 ACNGTGGTCG GGGTGGCCTG TTACGCCGTT GTCNTCGAAC ACGAGTAGCA GGTCTGCTCC 780
 GGCGAGGGCA TCCACCACGC GTTGCCTCAG CTCGT 815

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAGCCGCC GGCTGAGGTC TCAGATCAGA GAGTCTCCGG ACTCACCGGG GCGGTTTCAGC 60
 CTTCTCCCAG AACAACTGCT GAAGATCCTC GCCCGCGAAA CAGGCGCTGA TTTGACGCTC 120
 TATGACCGGT TGAACGACGA GATCATCCGG CAGATTGATA TGGCACCGCT GGGCTAACAG 180
 GTGCGCAAGA TGGTGCAGCT GTATGTCTCG GACTCCGTGT CGCGGATCAG CTTTGCCGAC 240
 GGCCGGGTGA TCGTGTGGAG CGAGGAGCTC GGCGAGAGCC AGTATCCGAT CGAGACGCTG 300
 GACGGCATCA CGCTGTTTGG GCGGCCGACG ATGACAACGC CCTTCATCGT TGAGATGCTC 360
 AAGCGTGAGC GCGACATCCA GCTCTTCACG ACCGACGGCC ACTACCAGGG CCGGATCTCA 420
 ACACCCGACG TGTCATACGC GCCGCGGCTC CGTCAGCAAG TTCACCGCAC CGACGATCCT 480
 GCGTTCTGCC TGTCGTTAAG CAAGCGGATC GTGTCGAGGA AGATCCTGAA TCAGCAGGCC 540
 TTGATTGCGG CACACACGTC GGGGCAAGAC GTTGCTGAGA GCATCCGCAC GATGAAGCAC 600
 TCGCTGGCCT GGGTCGATCG ATCGGGCTCC CTGGCGGAGT TGAACGGGTT CGAGGGAAAT 660
 GCCGCAAAGG CATACTTAC CGCGCTGGGG CATCTCGTCC CGCAGGAGTT CGCATTCCAG 720
 GGCCGCTCGA CTCGGCCGCC GTTGGACGCC TTCAACTCGA TGGTCAGCCT CGGCTATTGC 780
 CTGCTGTACA AGAACATCAT AGGGGCGATC GAGCGTCACA GCCTGAACGC GTATATCGGT 840

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TTCCTACACC AGGATTCACG AGGGCACGCA ACGTCTCGTG CCGAATTCGG CACGAGCTCC 900
 GCTGAAACCG CTGGCCGGCT GCTCAGTGCC CGTACGTAAT CCGCTGCGCC CAGGCCGGCC 960
 CGCCGGCCGA ATACCAGCAG ATCGGACAGC GAATTGCCGC CCAGCCGGTT GGAGCCGTGC 1020
 ATACCGCCGG CACACTCACC GGCAGCGAAC AGGCCTGGCA CCGTGGCGGC GCCGGTGTCC 1080
 GCGTCTACTT CGACACCGCC CATCACGTAG TGACACGTCG GCCCGACTTC CATTCCTGC 1140
 GTTCGGCACG AG 1152

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 655 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTCGTGCCGA TTCGGCAGGG TGTACTTGCC GGTGGTGTAN GCCGCATGAG TGCCGACGAC 60
 CAGCAATGCG GCAACAGCAC GGATCCCGGT CAACGACGCC ACCCGGTCCA CGTGGGCGAT 120
 CCGCTCGAGT CCGCCCTGGG CGGCTCTTTC CTTGGGCAGG GTCATCCGAC GTGTTTCCGC 180
 CGTGGTTTGC CGCCATTATG CCGGCGCGCC GCGTCGGGCG GCCGGTATGG CCGAANGTCG 240
 ATCAGCACAC CCGAGATACG GGTCTGTGCA AGCTTTTTGA GCGTCGCGCG GGGCAGCTTC 300
 GCCGGCAATT CTACTAGCGA GAAGTCTGGC CCGATACGGA TCTGACCGAA GTCGCTGCGG 360
 TGCAGCCCAC CCTCATTGGC GATGGCGCCG ACGATGGCGC CTGGACCGAT CTTGTGCCGC 420
 TTGCCGACGG CGACGCGGTA GGTGGTCAAG TCCGGTCTAC GCTTGGGCCT TTGCGGACGG 480
 TCCCGACGCT GGTCGCGGTT GCGCCGCGAA AGCGGCGGGT CGGGTGCCAT CAGGAATGCC 540
 TCACCGCCGC GGCAGTGCAC GGCCAGTGCC GCGGCGATGT CAGCCATCGG GACATCATGC 600
 TCGCGTTCAT ACTCCTCGAC CAGTCGGCGG AACAGCTCGA TTCCCGGACC GCCCA 655

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val
 1 5 10 15
 Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu
 20 25 30
 Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr
 35 40 45
 Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Pro Asp Asp Pro Thr Ala
 50 55 60
 Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg
 65 70 75 80
 Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro
 85 90 95
 Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro
 100 105 110
 Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro
 115 120 125
 Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr
 130 135 140
 Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr
 145 150 155 160
 Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr
 165 170 175
 Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala
 180 185 190
 Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro
 195 200 205
 Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro
 210 215 220
 Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala
 225 230 235 240
 Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn
 245 250 255
 Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe
 260 265

(2) INFORMATION FOR SEQ ID NO:143:

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 205220" E4848001

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro
1           5           10           15

Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro
          20           25           30

Ser Pro Pro Thr Gly Trp Val Pro Arg Ala Leu Leu Pro Pro Trp Leu
          35           40           45

Ala Gly Thr Pro Pro Ala Pro Pro Val Pro Pro Met Ala Pro Leu Pro
          50           55           60

Pro Ala Ala Pro Leu Pro Pro Leu Pro Pro Leu Pro Pro Leu Pro Thr
65           70           75           80

Ser His Pro Pro Arg Pro Pro Ala Pro Pro Ala Pro Pro Ala Pro Pro
          85           90           95

Ala Cys Pro Phe Val Pro Val Pro Pro Ala Pro Pro Leu Pro Pro Ser
          100          105          110

Pro Pro Thr Glu Leu Pro Ala Asp Ala Ala Cys Pro Pro Ala Pro Pro
          115          120          125

Ala Pro Pro Leu Ala Pro Pro Ser Pro Pro Ala Gly Ser Ala Ala Ile
          130          135          140

Arg Ala Leu Thr Gly Ala Thr Ser Ala Ser Thr Leu Gly His Arg Ala
145          150          155          160

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly
          165          170

```

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

205220" E4B4B00T

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
 1 5 10 15
 Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
 20 25 30
 Asn Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
 1 5 10 15
 Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr
 20 25 30
 Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
 35 40 45
 Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
 50 55 60
 Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
 65 70 75 80
 Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
 85 90 95
 Gly Gln Leu Arg Arg Gln Phe Tyr
 100

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

10084843.022502

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAGAGAATTC TCAGAAGCCC ATTTGCGAGG ACA

33

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(ix) FEATURE:

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(A) NAME/KEY: CDS
(B) LOCATION: 152..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCCACCGA ACAGCTGTTG TCCTCGCCGA	60
AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCGGG GGACGTCAAG GACGCCAAGC	120
GCGGAAATTG AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG	172
Val Lys Ile Arg Leu His Thr	
1 5	
CTG TTG GCC GTG TTG ACC GCT GCG CCG CTG CTG CTA GCA GCG GCG GGC	220
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly	
10 15 20	
TGT GGC TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GCC	268
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala	
25 30 35	
GGT ACT GTC GCG ACT ACC CCC GCG TCG TCG CCG GTG ACG TTG GCG GAG	316
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu	
40 45 50 55	
ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCC	364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala	
60 65 70	
TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT	412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly	
75 80 85	
TCT GGT GCC GGG ATC GCG CAG GCC GCC GCC GGG ACG GTC AAC ATT GGG	460
Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly	
90 95 100	
GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCC GCG CAC AAG GGG	508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly	
105 110 115	
CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC	556
Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn	
120 125 130 135	
CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG	604
Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala	
140 145 150	
GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT	652
Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala	
155 160 165	
GCG CTC AAC CCC GGC GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG	700
Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu	

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170	175	180	
CAC CGC TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG			748
His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu			
185	190	195	
TCC AAG CAA GAT CCC GAG GGC TGG GGC AAG TCG CCC GGC TTC GGC ACC			796
Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr			
200	205	210	215
ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC			844
Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn			
220	225	230	
GGC GGC ATG GTG ACC GGT TGC GCC GAG ACA CCG GGC TGC GTG GCC TAT			892
Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr			
235	240	245	
ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CGG GGA CTC GGC GAG			940
Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu			
250	255	260	
GCC CAA CTA GGC AAT AGC TCT GGC AAT TTC TTG TTG CCC GAC GCG CAA			988
Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln			
265	270	275	
AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC CCG GCG AAC			1036
Ser Ile Gln Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn			
280	285	290	295
CAG GCG ATT TCG ATG ATC GAC GGG CCC GCC CCG GAC GGC TAC CCG ATC			1084
Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile			
300	305	310	
ATC AAC TAC GAG TAC GCC ATC GTC AAC AAC CGG CAA AAG GAC GCC GCC			1132
Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala			
315	320	325	
ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GGC			1180
Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly			
330	335	340	
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC			1228
Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro			
345	350	355	
GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC			1273
Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser			
360	365	370	
TAGCCTCGTT GACCACCACG CGACAGCAAC CTCCGTCGGG CCATCGGGCT GCTTTGCGGA			1333
GCATGCTGGC CCGTGCCGGT GAAGTCGGCC GCGCTGGCCC GGCCATCCGG TGGTTGGGTG			1393
GGATAGGTGC GGTGATCCCG CTGCTTGCGC TGGTCTTGGT GCTGGTGGTG CTGGTCATCG			1453

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AGGCGATGGG TGCGATCAGG CTCAACGGGT TGCATTTCTT CACCGCCACC GAATGGAATC 1513
 CAGGCAACAC CTACGGCGAA ACCGTTGTCA CCGACGCGTC GCCCATCCGG TCGGCGCCTA 1573
 CTACGGGGCG TTGCCGCTGA TCGTCGGGAC GCTGGCGACC TCGGCAATCG CCCTGATCAT 1633
 CGCGGTGCCG GTCTCTGTAG GAGCGGCGCT GGTGATCGTG GAACGGCTGC CGAAACGGTT 1693
 GGCCGAGGCT GTGGGAATAG TCCTGGAATT GCTCGCCGGA ATCCCCAGCG TGGTCGTCGG 1753
 TTTGTGGGGG GCAATGACGT TCGGGCCGTT CATCGCTCAT CACATCGCTC CGGTGATCGC 1813
 TCACAACGCT CCCGATGTGC CGGTGCTGAA CTACTTGCGC GGCGACCCGG GCAACGGGGA 1873
 GGGCATGTTG GTGTCCGGTC TGGTGTGGC GGTGATGGTC GTTCCCATTA TCGCCACCAC 1933
 CACTCATGAC CTGTTCCGGC AGGTGCCGGT GTTGCCCCGG GAGGGCGCGA TCGGGAATTC 1993

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Val Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1 5 10 15
 Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20 25 30
 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35 40 45
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50 55 60
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65 70 75 80
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys

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130		135		140
Leu Asn Gly Lys Val	Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr			
145	150	155		160
Trp Asp Asp Pro Gln	Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro			
	165	170		175
Gly Thr Ala Val Val	Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr			
	180	185		190
Phe Leu Phe Thr Gln Tyr	Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly			
	195	200		205
Lys Ser Pro Gly Phe Gly	Thr Thr Val Asp Phe Pro Ala Val Pro Gly			
	210	215		220
Ala Leu Gly Glu Asn Gly	Asn Gly Gly Met Val Thr Gly Cys Ala Glu			
	225	230		235
Thr Pro Gly Cys Val Ala	Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala			
	245	250		255
Ser Gln Arg Gly Leu Gly	Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn			
	260	265		270
Phe Leu Leu Pro Asp Ala	Gln Ser Ile Gln Ala Ala Ala Gly Phe			
	275	280		285
Ala Ser Lys Thr Pro Ala	Asn Gln Ala Ile Ser Met Ile Asp Gly Pro			
	290	295		300
Ala Pro Asp Gly Tyr Pro	Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn			
	305	310		315
Asn Arg Gln Lys Asp Ala	Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu			
	325	330		335
His Trp Ala Ile Thr Asp	Gly Asn Lys Ala Ser Phe Leu Asp Gln Val			
	340	345		350
His Phe Gln Pro Leu Pro	Pro Ala Val Val Lys Leu Ser Asp Ala Leu			
	355	360		365
Ile Ala Thr Ile Ser Ser				
	370			

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA	CGGCAGGCTG	GTGGAGGAAG	GGCCCACCGA	ACAGCTGTTT	TCCTCGCCGA	60
AGCATGCGGA	AACCGCCCGA	TACGTCGCCG	GACTGTCGGG	GGACGTCAAG	GACGCCAAGC	120
GCGGAAATTG	AAGAGCACAG	AAAGGTATGG	CGTGAAAATT	CGTTTGCATA	CGCTGTTGGC	180
CGTGTTGACC	GCTGCGCCGC	TGCTGCTAGC	AGCGGCGGGC	TGTGGCTCGA	AACCACCGAG	240
CGGTTGCGCT	GAAACGGGCG	CCGGCGCCGG	TACTGTCGCG	ACTACCCCCG	CGTCGTCGCC	300
GGTGACGTTG	GCGGAGACCG	GTAGCACGCT	GCTCTACCCG	CTGTTCAACC	TGTGGGGTCC	360
GGCCTTTTAC	GAGAGGTATC	CGAACGTCAC	GATCACCGCT	CAGGGCACCG	GTTCTGGTGC	420
CGGGATCGCG	CAGGCCGCCG	CCGGGACGGT	CAACATTGGG	GCCTCCGACG	CCTATCTGTC	480
GGAAGGTGAT	ATGGCCGCGC	ACAAGGGGCT	GATGAACATC	GCGCTAGCCA	TCTCCGCTCA	540
GCAGGTCAAC	TACAACCTGC	CCGGAGTGAG	CGAGCACCTC	AAGCTGAACG	GAAAAGTCCT	600
GGCGGCCATG	TACCAGGGCA	CCATCAAAAC	CTGGGACGAC	CCGCAGATCG	CTGCGCTCAA	660
CCCCGGCGTG	AACCTGCCCC	GCACCGCGGT	AGTTCCGCTG	CACCGCTCCG	ACGGGTCCGG	720
TGACACCTTC	TTGTTTACCC	AGTACCTGTC	CAAGCAAGAT	CCCGAGGGCT	GGGGCAAGTC	780
GCCCCGGCTT	GGCACCACCG	TCGACTTCCC	GGCGGTGCCG	GGTGCGCTGG	GTGAGAACGG	840
CAACGGCGGC	ATGGTGACCG	GTTGCGCCGA	GACACCGGGC	TGCGTGCCCT	ATATCGGCAT	900
CAGCTTCCTC	GACCAGGCCA	GTCAACGGGG	ACTCGGCGAG	GCCCAACTAG	GCAATAGCTC	960
TGGCAATTTT	TTGTTGCCCG	ACGCGCAAAG	CATTGAGGCC	GCGGCGGCTG	GCTTCGCATC	1020
GAAAACCCCC	GCGAACCAGG	CGATTTTCGAT	GATCGACGGG	CCCGCCCCCG	ACGGCTACCC	1080
GATCATCAAC	TACGAGTACG	CCATCGTCAA	CAACCGGCAA	AAGGACGCCG	CCACCGCGCA	1140
GACCTTGCA	GCATTTCTGC	ACTGGGCGAT	CACCGACGGC	AACAAGGCCT	CGTTCCTCGA	1200
CCAGGTTCAT	TTCCAGCCGC	TGCCGCCCGC	GGTGGTGAAG	TTGTCTGACG	CGTTGATCGC	1260
GACGATTTCC	AGCTAGCCTC	GTTGACCACC	ACGCGACAGC	AACCTCCGTC	GGGCCATCGG	1320
GCTGCTTTGC	GGAGCATGCT	GGCCCGTGCC	GGTGAAGTCG	GCCGCGCTGG	CCCGGCCATC	1380
CGGTGGTTGG	GTGGGATAGG	TGCGGTGATC	CCGCTGCTTG	CGCTGGTCTT	GGTGCTGGTG	1440
GTGCTGGTCA	TCGAGGCGAT	GGGTGCGATC	AGGCTCAACG	GGTTGCATTT	CTTCACCGCC	1500
ACCGAATGGA	ATCCAGGCAA	CACCTACGGC	GAAACCGTTG	TCACCGACGC	GTCGCCCATC	1560
CGGTCGGCGC	CTACTACGGG	GCGTTGCCGC	TGATCGTCGG	GACGCTGGCG	ACCTCGGCAA	1620

TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC 1680
 TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCCTGGA ATTGCTCGCC GGAATCCCCA 1740
 GCGTGGTCGT CGGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG 1800
 CTCCGGTGAT CGCTCACAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC 1860
 CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTT GGCGGTGATG GTCGTTCCCA 1920
 TTATCGCCAC CACCACTCAT GACCTGTTCC GGCAGGTGCC GGTGTTGCCC CGGGAGGGCG 1980
 CGATCGGGAA TTC 1993

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met	Lys	Ile	Arg	Leu	His	Thr	Leu	Leu	Ala	Val	Leu	Thr	Ala	Ala	Pro	1	5	10	15
Leu	Leu	Leu	Ala	Ala	Ala	Gly	Cys	Gly	Ser	Lys	Pro	Pro	Ser	Gly	Ser	20	25	30	
Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	Ala	Ser	35	40	45	
Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	Pro	Leu	50	55	60	
Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	Val	Thr	65	70	75	80
Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	Ala	Ala	85	90	95	
Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	Glu	Gly	100	105	110	
Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	Ile	Ser	115	120	125	
Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His	Leu	Lys	130	135	140	
Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile	Lys	Thr	145	150	155	160

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Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGTCTTGACC ACCACCTGGG TGTCGAAGTC GGTGCCCCGA TTGAAGTCCA GGTACTCGTG 60
 GGTGGGGCGG GCGAAACAAT AGCGACAAGC ATGCGAGCAG CCGCGGTAGC CGTTGACGGT 120

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GTAGCGAAAC	GGCAACGCGG	CCGCGTTGGG	CACCTTGTTT	AGCGCTGATT	TGCACAACAC	180
CTCGTGGAAG	GTGATGCCGT	CGAATTGTGG	CGCGCGAACG	CTGCGGACCA	GGCCGATCCG	240
CTGCAACCCG	GCAGCGCCCG	TCGTCAACGG	GCATCCCGTT	CACCGCGACG	GCTTGCCGGG	300
CCCAACGCAT	ACCATATTTC	GAACAACCGT	TCTATACTTT	GTCAACGCTG	GCCGCTACCG	360
AGCGCCGCAC	AGGATGTGAT	ATGCCATCTC	TGCCCCGACA	GACAGGAGCC	AGGCCTTATG	420
ACAGCATTCG	GCGTCGAGCC	CTACGGGCAG	CCGAAGTACC	TAGAAATCGC	CGGGAAGCGC	480
ATGGCGTATA	TCGACGAAGG	CAAGGGTGAC	GCCATCGTCT	TTCAGCACGG	CAACCCACG	540
TCGTCTTACT	TGTGGGCGAA	CATCATGCGG	CACCTTGAAG	GGCTGGGCGG	GCTGGTGGCC	600
TGCGATCTGA	TCGGGATGGG	CGCGTCGGAC	AAGCTCAGCC	CATCGGGACC	CGACCGCTAT	660
AGCTATGGCG	AGCAACGAGA	CTTTTTGTTC	GCGCTCTGGG	ATGCGCTCGA	CCTCGGCGAC	720
CACGTGGTAC	TGGTGCTGCA	CGACTGGGGC	TCGGCGCTCG	GCTTCGACTG	GGCTAACCAG	780
CATCGCGACC	GAGTGCAGGG	GATCGCGTTC	ATGGAAGCGA	TCGTCACCCC	GATGACGTGG	840
GCGGACTGGC	CGCCGGCCGT	GCGGGGTGTG	TTCCAGGGTT	TCCGATCGCC	TCAAGGCGAG	900
CCAATGGCGT	TGGAGCACAA	CATCTTTGTC	GAACGGGTGC	TGCCCCGGGC	GATCCTGCGA	960
CAGCTCAGCG	ACGAGGAAAT	GAACCACTAT	CGGCGGCCAT	TCGTGAACGG	CGGCGAGGAC	1020
CGTCGCCCCA	CGTTGTCTGT	GCCACGAAAC	CTTCCAATCG	ACGGTGAGCC	CGCCGAGGTC	1080
GTCGCGTTGG	TCAACGAGTA	CCGGAGCTGG	CTCGAGGAAA	CCGACATGCC	GAAACTGTTC	1140
ATCAACGCCG	AGCCCGGCGC	GATCATCACC	GGCCGCATCC	GTGACTATGT	CAGGAGCTGG	1200
CCCAACCAGA	CCGAAATCAC	AGTGCCCGGC	GTGCATTTTC	TTCAGGAGGA	CAGCGATGGC	1260
GTCGTATCGT	GGGCGGGCGC	TCGGCAGCAT	CGGCGACCTG	GGAGCGCTCT	CATTTACGA	1320
GACCAAGAAT	GTGATTTCCG	GCGAAGGCGG	CGCCCTGCTT	GTCAACTCAT	AAGACTTCCT	1380
GCTCCGGGCA	GAGATTCTCA	GGGAAAAGGG	CACCAATCGC	AGCCGCTTCC	TTCGCAACGA	1440
GGTCGACAAA	TATACGTGGC	AGGACAAAGG	TCTTCCTATT	TGCCCAGCGA	ATTAGTCGCT	1500
GCCTTTCTAT	GGGCTCAGTT	CGAGGAAGCC	GAGCGGATCA	CGCGTATCCG	ATTGGACCTA	1560
TGGAACCGGT	ATCATGAAAG	CTTCGAATCA	TTGGAACAGC	GGGGGCTCCT	GCGCCGTCCG	1620
ATCATCCAC	AGGGCTGCTC	TCACAACGCC	CACATGTACT	ACGTGTTACT	AGCGCCCAGC	1680
GCCGATCGGG	AGGAGGTGCT	GGCGCGTCTG	ACGAGCGAAG	GTATAGGCGC	GGTCTTTTCAT	1740

TACGTGCCGC TTCACGATTC GCCGGCCGGG CGTCGCT

1777

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAGATTGAAT CGTACCGGTC TCCTTAGCGG CTCCGTCCCG TGAATGCCCA TATCACGCAC	60
GGCCATGTTC TGGCTGTCTGA CCTTCGCCCC ATGCCCGGAC GTTGGTAAAC CCAGGGTTTG	120
ATCAGTAATT CCGGGGGACG GTTGCGGGAA GCGCGCCAGG ATGTGCGTGA GCCGCGGCGC	180
CGCCGTCGCC CAGGCGACCG CTGGATGCTC AGCCCCGGTG CGGCGACGTA GCCAGCGTTT	240
GGCGCGTGTC GTCCACAGTG GTACTCCGGT GACGACGCGG CGCGGTGCCT GGGTGAAGAC	300
CGTGACCGAC GCCGCCGATT CAGA	324

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GCGGTACCGC CGCGTTGCGC TGGCACGGGA CCTGTACGAC CTGAACCACT TCGCCTCGCG	60
AACGATTGAC GAACCGCTCG TCGGGCGGCT GTGGGTGCTC AAGGTGTGGG GTGATGTCGT	120
CGATGACCGG CGCGGCACCC GGCCACTACG CGTCGAAGAC GTCCTCGCCG CCCGCAGCGA	180
GCACGACTTC CAGCCCGACT CGATCGGCGT GCTGACCCGT CCTGTCGCTA TGGCTGCCTG	240
GGAAGCTCGC GTTCGGAAGC GATTTGCGTT CCTCACTGAC CTCGACGCCG ACGAGCAGCG	300
GTGGGCCCGC TGCACGAAC GGCACCGCCG CGAAGTGGAG AACGCGCTGG CGGTGCTGCG	360
GTCCTGATCA ACCTGCCGGC GATCGTGCCG TTCCGCTGGC ACGGTTGCGG CTGGACGCGG	420
CTGAATCGAC TAGATGAGAG CAGTTGGGCA CGAATCCGGC TGTGGTGGTG AGCAAGACAC	480
GAGTACTGTC ATCACTATTG GATGCACTGG ATGACCGGCC TGATTGAGCA GGACCAATGG	540
AACTGCCCCG GGCAAAACGT CTCGGAGATG ATCGGCGTCC CCTCGGAACC CTGCGGTGCT	600
GGCGTCATTC GGACATCGGT CCGGCTCGCG GGATCGTGGT GACGCCAGCG CTGAAGGAGT	660

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GGAGCGCGGC GGTGCACGCG CTGCTGGACG GCCGGCAGAC GGTGCTGCTG CGTAAGGGCG 720
 GGATCGGCGA GAAGCGCTTC GAGGTGGCGG CCCACGAGTT CTTGTTGTTC CCGACGGTCG 780
 CGCACAGCCA CGCCGAGCGG GTTCGCCCCG AGCACC GCGA CCTGCTGGGC CCGGCGGCCG 840
 CCGACAGCAC CGACGAGTGT GTGCTACTGC GGGCCGCAGC GAAAGTTGTT GCCGCACTGC 900
 CGGTTAACCG GCCAGAGGGT CTGGACGCCA TCGAGGATCT GCACATCTGG ACCGCCGAGT 960
 CGGTGCGCGC CGACCGGCTC GACTTTCGGC CCAAGCACAA ACTGGCCGTC TTGGTGGTCT 1020
 CGGCGATCCC GCTGGCCGAG CCGGTCCGGC TGGCGCGTAG GCCCAGTAC GGCGGTTGCA 1080
 CCAGCTGGGT GCAGCTGCCG GTGACGCCGA CGTTGGCGGC GCCGGTGAC GACGAGGCCG 1140
 CGCTGGCCGA GGTGCGCCGCC CGGGTCCGCG AGGCCGTGGG TTGACTGGGC GGCATCGCTT 1200
 GGGTCTGAGC TGTACGCCCA GTCGGCGCTG CGAGTGATCT GCTGTCGGTT CGGTCCCTGC 1260
 TGGCGTCAAT TGACGGCGCG GGCAACAGCA GCATTGGCGG CGCCATCCTC CGCGCGGCCG 1320
 GCGCCCACCG CTACAACC 1338

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CCGGCGGCAC CGGCGGCACC GCGGTACCG GCGGCAACGG CGCTGACGCC GCTGCTGTGG 60
 TGGGCTTCGG CGCGAACGGC GACCCTGGCT TCGCTGGCGG CAAAGGCGGT AACGGCGGAA 120
 TAGGTGGGGC CGCGGTGACA GCGGGGTCG CCGGCGACGG CGGCACCGGC GGCAAAGGTG 180
 GCACCGGCGG TGCCGGCGGC GCCGGCAACG ACGCCGGCAG CACCGGCAAT CCCGGCGGTA 240
 AGGGCGGCGA CGGCGGGATC GCGGTGCCG GCGGGGCCG CGGCGCGGCC GGCACCGGCA 300
 ACGGCGGCCA TGCCGGCAAC C 321

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GAAGACCCGG CCCC GCCATA TCGATCGGCT CGCCGACTAC TTTCGCCGAA CGTGCACGCG 60
 GCGGCGTCGG GCTGATCATC ACCGGTGGCT ACGCGCCCAA CCGCACC GGA TGGCTGCTGC 120
 CGTTCGCCTC CGAACTCGTC ACTTCGGCGC AAGCCCGACG GCACCGCCGA ATCACCAGGG 180
 CGGTCCACGA TTCGGGTGCA AAGATCCTGC TGCAAATCCT GCACGCCGGA CGCTACGCCT 240
 ACCACCCACT TCGGGTCAGC GCCTCGCCGA TCAAGGCGCC GATCACCCCG TTTCGTCCGC 300
 GAGCACTATC GGCTCGCGGG GTCGAAGCGA CCATCGCGGA TTTCGCCCGC TGC GCGCAGT 360
 TGGCCCGCGA TGCCGGCTAC GACGGCGTCG AAATCATGGG CAGCGAAGGG TATCTGCTCA 420
 ATCAGTTCTT GGC GCCGCGC ACCAACAAGC GCACCGACTC GTGGGGCGGC ACACCGGCCA 480
 ACCGTCGCCG GT 492

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Phe Ala Gln His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala
 1 5 10 15
 Asn Ala Ala Asp Gln Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg
 20 25 30
 Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr
 35 40 45
 His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Gln Arg Trp Pro Leu Pro
 50 55 60
 Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Glu
 65 70 75 80
 Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys
 85 90 95
 Tyr Leu Glu Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys
 100 105 110
 Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu
 115 120 125
 Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala

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130	135	140
Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly 145 150 155 160		
Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu 165 170 175		
Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp 180 185 190		
Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg 195 200 205		
Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp 210 215 220		
Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser 225 230 235 240		
Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg 245 250 255		
Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn 260 265 270		
His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr 275 280 285		
Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val 290 295 300		
Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met 305 310 315 320		
Pro Lys Leu Phe Ile Asn Ala Glu Pro Gly Ala Ile Ile Thr Gly Arg 325 330 335		
Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val 340 345 350		
Pro Gly Val His Phe Val Gln Glu Asp Ser Asp Gly Val Val Ser Trp 355 360 365		
Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg 370 375 380		
Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Arg Pro Ala Cys Gln Leu 385 390 395 400		
Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln 405 410 415		
Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly 420 425 430		

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Gln Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp
 435 440 445
 Ala Gln Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu
 450 455 460
 Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Gln Arg Gly Leu
 465 470 475 480
 Leu Arg Arg Pro Ile Ile Pro Gln Gly Cys Ser His Asn Ala His Met
 485 490 495
 Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala
 500 505 510
 Arg Leu Thr Ser Glu Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu
 515 520 525
 His Asp Ser Pro Ala Gly Arg Arg
 530 535

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Asn Glu Ser Ala Pro Arg Ser Pro Met Leu Pro Ser Ala Arg Pro Arg
 1 5 10 15
 Tyr Asp Ala Ile Ala Val Leu Leu Asn Glu Met His Ala Gly His Cys
 20 25 30
 Asp Phe Gly Leu Val Gly Pro Ala Pro Asp Ile Val Thr Asp Ala Ala
 35 40 45
 Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Gln Phe Arg His Val
 50 55 60
 Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Gln Arg Asp Asp Leu
 65 70 75 80
 Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Gln Arg Gly
 85 90 95
 Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His
 100 105 110
 Phe Leu Val Ala Glu Leu Ser Gln Asp Arg Pro Gly Gln His Pro Phe
 115 120 125

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Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser
 130 135 140
 Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg
 145 150 155 160
 His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val
 165 170 175
 Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val
 180 185 190
 Gln His Gln Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg
 195 200 205
 Glu Gln Lys Val Ser Leu Leu Ala Ile Ala Ile Ala Val Gly Ser Arg
 210 215 220
 Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His
 225 230 235 240
 Gln Pro Ala Gln Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val
 245 250 255
 Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala
 260 265 270
 Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe
 275 280

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

ATGAACATGT CGTCGGTGGT GGGTCGCAAG GCCTTTGCGC GATTCGCCCG CTACTCCTCC	60
GCCATGCACG CGATCGCCGG TTTCTCCGAT GCGTTGCGCC AAGAGCTGCG GGGTAGCGGA	120
ATCGCCGTCT CGGTGATCCA CCCGGCGCTG ACCCAGACAC CGCTGTTGGC CAACGTGCAC	180
CCCGCCGACA TGCCGCCGCC GTTTCGCAGC CTCACGCCCA TTCCCGTTCA CTGGGTGCGC	240
GCAGCGGTGC TTGACGGTGT GGCG	264

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs

205220" 84848001

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TAGTCGGCGA CGATGACGTC GCGGTCCAGG CCGACCGCTT CAAGCACCAG CGCGACCACG	60
AAGCCGGTGC GATCCTTACC CGCGAAGCAG TGGGTGAGCA CCGGGCGTCC GGCGGCAAGC	120
AGTGTGACGA CACGATGTAG CGCGCGCTGT GCTCCATTGC GCGTTGGGAA TTGGCGATAC	180
TCGTCGGTCA TGTAGCGGGT GGCCGCGTCA TTTATCGACT GGCTGGATTG GCCGGACTCG	240
CCGTTGGACC CGTCATTGGT TAGCAGCCTC TTGAATGCGG TTTCGTGCGG CGCTGAGTCG	300
TCGGCGTCAT CATCGGCGAG GTCGGGGAAC GGCAGCAGGT GGACGTCGAT GCCGTCCGGA	360
ACCCGTCCTG GACCGCGGCG GGCAACCTCC CGGGACGACC GCAGGTCGGC AACGTCGGTG	420
ATCCCCAGCC GGCGCAGCGT TGCCCCCTCGT GCCGAATTCG GCACGAGGCT GGCGAGCCAC	480
CGGGCATCAC CAAGCAACGC TTGCCCAGTA CGGATCGTCA CTTCCGCATC CGGCAGACCA	540
ATCTCCTCGC CGCCCATCGT CAGATCCCGC TCGTGCGTTG ACAAGAACGG CCGCAGATGT	600
GCCAGCGGGT ATCGGAGATT GAACCGCGCA CGCAGTTCTT CAATCGCTGC GCGCTGCCGC	660
ACTATTGGCA CTTTCCGGCG GTCGCGGTAT TCAGCAAGCA TCGAGTCTC GACGAACTCG	720
CCCCACGTAA CCCACGGCGT AGCTCCCGGC GTGACGCGGA GGATCGGCGG GTGATCTTTG	780
CCGCCACGCT CGTAGCCGTT GATCCACCGC TTCGCGGTGC CGGCGGGGAG GCCGATCAGC	840
TTATCGACCT CGGCGTATGC CGACGGCAAG CTGGGCGCGT TCGTCGAGGT CAAGAACTCC	900
ACCATCGGCA CCGGCACCAA GGTGCCGCAC CTGACCTACG TCGGCGACGC CGACATCGGC	960
GAGTACAGCA ACATCGGCGC CTCCAGCGTG TTCGTCAACT ACGACGGTAC GTCCAAACGG	1020
CGCACCACCG TCGGTTCGCA CGTACGGACC GGGTCCGACA CCATGTTTCGT GGCCCCAGTA	1080
ACCATCGGCG ACGGCGCGTA TACCGGGGCC GGCACAGTGG TGCGGGAGGA TGTCCCGCCG	1140
GGGGCGCTGG CAGTGTCGGC GGGTCCGCAA C	1171

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

205220" 5484800T

GCAAAGGCGG CACCGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCCAAG 60
 ACGGCGGCCA AGGCGGCACC GGCGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT 120
 TCACCCAAGG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GGCGGCAACG 180
 GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCC 227

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CCTCGCCACC ATGGGCGGGC AGGGCGGTAG CGGTGGCGCC GGCTCTACCC CAGGCGCCAA 60
 GGGCGCCAC GGCTTCACTC CAACCAGCGG CGGCGACGGC GGCACGGCG GCAACGGCGG 120
 CAACTCCCAA GTGGTCGGCG GCAACGGCGG CGACGGCGGC AATGGCGGCA ACGGCGGCAG 180
 CGCCGGCACG GGCGGCAACG GCGGCCGCGG CGGCGACGGC GCGTTTGGTG GCATGAGTGC 240
 CAACGCCACC AACCCTGGTG AAAACGGGCC AAACGGTAAC CCCGGCGGCA ACGGTGGCGC 300
 CGGC 304

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GTGGGACGCT GCCGAGGCTG TATAACAAGG ACAACATCGA CCAGCGCCGG CTCGGTGAGC 60
 TGATCGACCT ATTTAACAGT GCGCGCTTCA GCCGGCAGGG CGAGCACCGC GCCCGGGATC 120
 TGATGGGTGA GGTCTACGAA TACTTCCTCG GCAATTTTCG TCGCGCGGAA GGGAAGCGGG 180
 GTGGCGAGTT CTTTACCCCG CCCAGCGTGG TCAAGGTGAT CGTGGAGGTG CTGGAGCCGT 240
 CGAGTGGGCG GGTGTATGAC CCGTGCTGCG GTTCCGGAGG CATGTTTGTG CAGACCGAGA 300
 AGTTCATCTA CGAACACGAC GGCGATCCGA AGGATGTCTC GATCTATGGC CAGGAAAGCA 360
 TTGAGGAGAC CTGGCGGATG GCGAAGATGA ACCTCGCCAT CCACGGCATC GACAACAAGG 420

GGCTCGGCGC CCGATGGAGT GATACCTTCG CCCGCGACCA GCACCCGGAC GTGCAGATGG 480
 ACTACGTGAT GGCCAATCCG CCGTTCAACA TCAAAGACTG GGCCCGCAAC GAGGAAGACC 540
 CACGCTGGCG CTTGGGTGTT CCGCCCGCCA ATAACGCCAA CTACGCATGG ATTCAGCACA 600
 TCCTGTACAA CTTGGCGCCG GGAGGTCGGG CGGGCGTGGT GATGGCCAAC GGGTCGATGT 660
 CGTCGAACTC CAACGGCAAG GGGGATATTC GCGCGCAAAT CGTGGAGGCG GATTTGTTT 720
 CCTGCATGGT CGCGTTACCC ACCCAGCTGT TCCGCAGCAC CGGAATCCCG GTGTGCCTGT 780
 GGTTTTTTCG CAAAAACAAG GCGGCAGGTA AGCAAGGGTC TATCAACCGG TCGGGGCAGG 840
 TGCTGTTTCAT CGACGCTCGT GAACTGGGCG ACCTAGTGGA CCGGGCCGAG CGGGCGCTGA 900
 CCAACGAGGA GATCGTCCGC ATCGGGGATA CCTTCCACGC GAGCACGACC ACCGGCAACG 960
 CCGGCTCCGG TGGTGCCGGC GGTAATGGGG GCACTGGCCT CAACGGCGCG GCGGTGCTG 1020
 GCGGGGCCCG CGGCAACGCG GGTGTCGCCG GCGTGTCTT CGGCAACGCT GTGGGCGGCG 1080
 ACGGCGGCAA CGGCGGCAAC GCGGGCCACG GCGGCGACGG CACGACGGGC GCGCCGGCG 1140
 GCAAGGGCGG CAACGGCAGC AGCGGTGCCG CCAGCGGCTC AGGCGTCGTC AACGTCACCG 1200
 CCGGCCACGG CGGCAACGGC GGCAATGGCG GCAACGGCGG CAACGGCTCC GCGGGCGCCG 1260
 GCGGCCAGGG CGGTGCCGGC GGCAGCGCCG GCAACGGCGG CCACGGCGGC GGTGCCACCG 1320
 GCGGCGCCAG CGGCAAGGGC GGCAACGGCA CCAGCGGTGC CGCCAGCGGC TCAGGCGTCA 1380
 TCAACGTCAC CGCCGGCCAC GCGGGCAACG GCGGCAATGG CCGCAACGGC GGCAACGGC 1439

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGGCCGGCGG GGCCGGATTT TCTCGTGCCT TGATTGTCGC TGGGGATAAC GGCGGTGATG 60
 GTGGTAACGG CGGGATGGGC GGGGCTGGCG GGGCTGGCGG CCCC GGCGGG GCCGGCGGCC 120
 TGATCAGCCT GCTGGGCGGC CAAGGCGCCG GCGGGGCCCG CGGGACCGGC GGGGCCGGCG 180
 GTGTTGGCGG TGACGGCGGG GCCGGCGGCC CCGGCAACCA GGCCTTCAAC GCAGGTGCCG 240
 GCGGGGCCCG CGGCCTGATC AGCCTGCTGG GCGGCCAAGG CGCCGGCGGG GCCGGCGGGA 300
 CCGGCGGGGC CGGCGGTGTT GGCGGTGAC 329

10084843.022502

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GCAACGGTGG CAACGGCGGC ACCAGCACGA CCGTGGGGAT GGCCGGAGGT AACTGTGGTG	60
CCGCCGGGCT GATCGGCAAC	80

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGGCTGTGTC GCACTCACAC CGCCGCATTC GGCACGTTG GCCGCCCAAT ATCCAGCTCA	60
AGGCCTACTA CTTACCGTCG GAGGACCGCC GCATCAAGGT GCGGGTCAGC GCCCAAGGAA	120
TCAAGGTCAT CGACCGCGAC GGGCATCGAG GCCGTCGTCG CGCGGCTCGG GCAGGATCCG	180
CCCCGGCGCA CTTGCGCGCG CAAGCGGGCT CATCGCTCCG AACGGCGGCG ATCCTGTGAG	240
CACAACTGAT GGC CGCAAC GAGATTCGTC CAATTGTCAA GCCGTGTTTCG ACCGCAGGGA	300
CCGGTTATAC GATGTCAAC CTATGTCACT CGCAAGAACC GGCATAACGA TCCCCTGATC	360
CGCCGACAGC CCACGAGTGC AAGACCGTTA CA	392

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

ACCGGCGCCA CCGGCGGCAC CGGGTTCGCC GGTGGCGCCG GCGGGGCCGG CGGGCAGGGC	60
GGTATCAGCG GTGCCGGCGG CACCAACGGC TCTGGTGGCG CTGGCGGCAC CGGCGGACAA	120
GGCGGCGCCG GGGGCGCTGG CGGGGCCGGC GCCGATAACC CCACCGGCAT CGGCGGCGCC	180

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GGCGGCACCG GCGGCACCGG CGGAGCGGCC GGAGCCGGCG GGGCCGGTGG CGCCATCGGT 240
 ACCGGCGGCA CCGGCGGCGC GGTGGGCAGC GTCGGTAACG CCGGGATCGG CGGTACCGGC 300
 GGTACGGGTG GTGTCGGTGG TGCTGGTGGT GCAGGTGCGG CTGCGGCCGC TGGCAGCAGC 360
 GCTACCGGTG GCGCCGGGTT CGCCGGCGGC GCCGGCGGAG AAGGCGGACC GGGCGGCAAC 420
 AGCGGTGTGG GCGGCACCAA CGGCTCCGGC GGCGCCGGCG GTGCAGGCGG CAAGGGCGGC 480
 ACCGGAGGTG CCGGCGGGTC CGGCGCGGAC AACCCACCG GTGCTGGTTT CGCCG 535

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CCGACGTCGC CGGGGCGATA CGGGGGTCAC CGACTACTAC ATCATCCGCA CCGAGAATCG 60
 GCCGCTGCTG CAACCGCTGC GGGCGGTGCC GGTCATCGGA GATCCGCTGG CCGACCTGAT 120
 CCAGCCGAAC CTGAAGGTGA TCGTCAACCT GGGCTACGGC GACCCGAACT ACGGCTACTC 180
 GACGAGCTAC GCCGATGTGC GAACGCCGTT CGGGCTGTGG CCGAACGTGC CGCCTCAGGT 240
 CATCGCCGAT GCCCTGGCCG CCGGAACACA AGAAGGCATC CTTGACTTCA CGGCCGACCT 300
 GCAGGCGCTG TCCGCGCAAC CGCTACGCT CCCGCGAGATC CAGCTGCCGC AACCCGCCGA 360
 TCTGGTGGCC GCGGTGGCCG CCGCACCGAC GCCGGCCGAG GTGGTGAACA CGCTCGCCAG 420
 GATCATCTCA ACCAACTACG CCGTCCTGCT GCCACCGTG GACATCGCCC TCGCCTGGTC 480
 ACCACCCTGC CGCTGTACAC CACCCAACCTG TTCGTCAGGC AACTCGCTGC GGGCAATCTG 540
 ATCAACGCGA TCGGCTATCC CCTGGCGGCC ACCGTAGGTT TAGGCACGAT CGATAGCGGG 600
 CGGCGTGGA TGTCTACCC TCCTCGCGGC GGCCTCGGAC ACCGTTCGAA ACATCGAGGG 660
 CCTCGTCACC TAACGGATT CCGACGGCAT 690

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

10084343.022502

ACGGTGACGG CGGTACTGGC GGCGGCCACG GCGGCAACGG CGGGAATCCC GGGTGGCTCT 60
 TGGGCACAGC CGGGGGTGGC GGCAACGGTG GCGCCGGCAG CACCGGTACT GCAGGTGGCG 120
 GCTCTGGGGG CACCGGCGGC GACGGCGGGA CCGGCGGGCG TGGCGGCCTG TTAATGGGCG 180
 CCGGCGCCGG CGGGCACGGT GGCCTGGCG GCGCGGGCGG TGCCGGTGTC GACGGTGGCG 240
 GCGCCGGCGG GGCCGGCGGG GCCGGCGGCA ACGGCGGCGC CGGGGGTCAA GCCGCCCTGC 300
 TGTTCGGGCG CGGCGGCACC GGCGGAGCCG GCGGCTACGG CGGCGATGGC GGTGGCGGCG 360
 GTGACGGCTT CGACGGCACG ATGGCCGGCC TGGGTGGTAC CGGTGGC 407

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GATCGGTCAG CGCATCGCCC TCGGCGGCAA GCGATTCCGC GGTCTCACCG AAGAACATCG 60
 TGCACGCGGC GGCGCGGACC AGCCCGCTGC GCTGCGGCGC GTCGAACGCC TCCAGCAGGC 120
 ACAGCCAGTC CTTGGCGGCC TGCGAGGCGA ACACGTCGGT GTCACCGGTG TAGATCGCCG 180
 GGATGCCCCG CTCCGCCAAC GCATTCCGGC ACGCCGCGC GTCTTTGTGA TGCTCGACGA 240
 TCACCGCGAT GTCTGCGGCC ACCACGGGCC GCCCGGCGAA GGTGGCCCCG CTGGCCAGTA 300
 GCGCCGCGAC GTCGGCGGCC AGGTCGTCGG GGATGTGCCG GCGCAGCGCT CCGGCGCGAC 360
 GCCCGAAAAA CGACCCCTCA CCCAGCTGGG TCCCGCTGGC ATATCCCTTG CCGTCCTGGG 420
 CGATATTGGA CGCGCATGCC CCGACCGCGT ACAGGCCGGC CACCACCG 468

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGTGGTAACG GCGGCCAGGG TGGCATCGGC GGCGCCGGCG AGAGAGGCGC CGACGGCGCC 60
 GGCCCCAATG CTAACGGCGC AAACGGCGAG AACGGCGGTA GCGGTGGTAA CCGTGGCGAC 120

GGCGGCGCCG GCGGCAATGG CGGCGCGGGC GGCAACGCGC AGGCGGCCCG GTACACCGAC 180

GGCGCCACGG GCACCGGCGG CGACGGCGGC AACGGCGGC 219

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TAGCTCCGGC GAGGGCGGCA AGGGCGGCGA CGGTGGCCAC GGCGGTGACG GCGTCGGCGG 60
 CAACAGTTCC GTCACCCAAG GCGGCAGCGG CGGTGGCGGC GGCGCCGGCG GCGCCGGCGG 120
 CAGCGGCTTT TTCGGCGGCA AGGGCGGCTT CGGCGGCGAC GGCGGTCAGG GCGGCCCCAA 180
 CGGCGGCGGT ACCGTCGGCA CCGTGGCCCG TGGCGGCGGC AACGGCGGTG TCGGCGGCCG 240
 GGGCGGCGAC GGCCTCTTTG CCGGTGCCCG CGGCCAGGGC GGCCTCGGTG GGCAGGGCGG 300
 CAATGGCGGC GGCTCCACCG GCGGCAACGG CGGCCTTGGC GGCAGGGGCG GTGGCGGAGG 360
 CAACGCCCCG GCTCGTGCCG AATCCGGGCT GACCATGGAC AGCGCGGCCA AGTTCGCTGC 420
 CATCGCATCA GGCAGGTACT GCCCCGAACA CCTGGAACAT CACCCGAGTT AGCGGGGCGC 480
 ATTCCTGAT CACC 494

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGGCCGGTGG TGCCGCGGGC CAGCTCTTCA GCGCCGGAGG CGCGGCGGGT GCCGTTGGGG 60
 TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCCG AGCGGCCGGC GCCGACCCCC 120
 CCGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GGCCTCGGCG 180
 GCCAGAGCGG CAACGCCATT GCCGGCGGCA TCAACGGCTC 220

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATGGCGGCAA CGGGGGCCCC GCGGTGCTG GCGGGGCCGG CGACTACAAT TTCCAACGGC	60
GGGCAGGGTG GTGCCGGCGG CCAAGGCGGC CAAGGCGGCC TGGGCGGGGC AAGCACCACC	120
TGATCGGCCT AGCCGCACCC GGGAAAGCCG ATCCAACAGG CGACGATGCC GCCTTCCTTG	180
CCGCGTTGGA CCAGGCCGGC ATCACCTACG CTGACCCAGG CCACGCCATA ACGGCCGCCA	240
AGGCGATGTG TGGGCTGTGT GCTAACGGCG TAACAGGTCT ACAGCTGGTC GCGGACCTGC	300
GGGACTACAA TCCCGGGCTG ACCATGGACA GCGCGGCCAA GTTCGCTGCC ATCGCATCAG	360
GCGCGTACTG CCCCGAACAC CTGGAACA	388

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GCAAAGGCGG CACCGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCCAAG	60
ACGGCGGCCA AGGCGGCACC GCGGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT	120
TCACCCAAGG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GGCGGCAACG	180
GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCCGGC ACCACAGGCG	240
GCGACGGCGG GGCCGGCGGG GCCGGCGGAA CCGGCGGAAC CGGCGGAGCC GCCGGCACCG	300
GCACCGGCGG CCAACAAGGC AACGGCGGCA ACGGCGGCAC CGGCGGCAAA GGCGGCACCG	360
GCGGCGACGG TGCACTCTCA GGCAGCACCG GTGGTGCCGG	400

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 538 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GGCAACGGCG GCAACGGCGG CATCGCCGGC ATTGGGCGGC AACGGCGTTC CGGGACGGGC	60
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AGCGGCAACG GCGGCCAACG GCGGCAGCGG CGGCAACGGC GGCAACGCCG GCATGGGCGG 120
 CAACAGCGGC ACCGGCAGCG GCGACGGCGG TGCCGGCGGG AACGGCGGCG CGGCGGGCAC 180
 GGGCGGCACC GGCGGCGACG GCGGCCTCAC CGGTACTGGC GGCACCGGCG GCAGCGGTGG 240
 CACCGGCGGT GACGGCGGTA ACGGCGGCAA CGGAGCAGAT AACACCGCAA ACATGACTGC 300
 GCAGGCGGGC GGTGACGGTG GCAACGGCGG CGACGGTGGC TTCGGCGGCG GGGCCGGGGC 360
 CGGCGGCGGT GGCTTGACCG CTGGCGCCAA CGGCACCGGC GGGCAAGGCG GCGCCGGGCG 420
 CGATGGCGGC AACGGGGCCA TCGGCGGCCA CGGCCCACTC ACTGACGACC CCGGCGGCAA 480
 CGGGGGCACC GGCGGCAACG GCGGCACCGG CGGCACCGGC GGC GCGGGCA TCGGCAGC 538

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGGCCGGTGG TGCCGCGGGC CAGCTCTTCA GCGCCGAGG CGCGGCGGGT GCCGTTGGGG 60
 TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCGG AGCGGCCGGC GCCGACGCCC 120
 CCGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GGCGTCGGCG 180
 GCCACGGCGG CAACGCCATT GCCGGCGGCA TCAACGGCTC CGGTGGTGCC GGCGGCACC 239

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

AGCAGCGCTA CCGGTGGCGC CGGGTTCGCC GGC GGCGGCCG GCGGAGAAGG CGGAGCGGGC 60
 GGCAACAGCG GTGTGGGCGG CACCAACGGC TCCGGCGGCG CCGGCGGTGC AGGCGGCAAG 120
 GGCGGCACCG GAGGTGCCCG CGGGTCCGGC GCGGACAACC CCACCGGTGC TGGTTTCGCC 180
 GGTGGCGCCG GCGGCACAGG TGGCGCGGCC GGCGCCGGCG GGGCCGGCGG GGCGACCGGT 240
 ACCGGCGGCA CCGGCGGCGT TGTCGGCGCC ACCGGTAGTG CAGGCATCGG CGGGGCCGGC 300
 GGCCGCGGCG GTGACGGCGG CGATGGGGCC AGCGGTCTCG GCCTGGGCCT CTCCGGCTTT 360

GACGGCGGCC AAGGCGGCCA AGGCGGGGCC GCGGCAGCG CCGGCGCCGG CGGCATCAAC 420
 GGGGCCGGCG GGGCCGGCGG CAACGGCGGC GACGGCGGGG ACGGCGCAAC CGGTGCCGCA 480
 GGTCTCGGCG ACAACGGCGG GGTGGCGGT GACGGTGGGG CCGGTGGCGC CGCCGGCAAC 540
 GCGGCAACG CGGGCGTCGG CCTGACAGCC AAGGCCGGCG ACGGCGGCGC CGCGGGCAAT 600
 GCGGCAACG GGGGCGCCGG CCGTGCTGGC GGGGCCGGCG ACAACAATTT CAACGGCGGC 660
 CAGGGTGGTG CCGGCGGCCA AGGCGGCCAA GCGGCTTGG GCGGGGCAAG CACCACCTGA 720
 TCGGCCTAGC CGCACCCGGG AAAGCCGATC CAACAGGCGA CGATGCCGCC TTCCTTGCCG 780
 CGTTGGACCA GGCCGGCATC ACCTACGCTG ACCCAGGCCA CGCCATAACG GCCGCCAAGG 840
 CGATGTGTGG GCTGTGTGCT AACGGCGTAA CAGGTCTACA GCTGGTCGCG GACCTGCGGG 900
 AATACAATCC CGGGCTGACC ATGGACAGCG CGGCCAAGTT CGCTGCCATC GCATCAGGCG 960
 CGTACTGCCC CGAACACCTG GAACA 985

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC 60
 CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTTCG CGATGCCGGC 120
 ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTTCAGT TTAGCGACGA TAATGGCTAT 180
 AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG 240
 AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCAGTGGC GGACCCACCG ACTGATGTCC 300
 CCATCACACC GTGCGAACTC ACGGCGGCTA AAAACGCCGC CCAACAGCTG GTATTGTCCG 360
 CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAAGA GCGGCAGCGT CTGGCGACCT 420
 CGCTGCGCAA CGCGGCCAAG GCGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG 480
 ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCCG GGCCGTCGGA GGGGACAGTT 540
 CGGCCGAACT AACCAGTACG CCGAGGGTGG CCACGGCCCG TGAACCCAAC TTCATGGATC 600
 TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTTTG 660

CGGATGGGTG GAACACTTTC AACCTGACGC TGCAAGGCGA CGTCAAGCGG TTCCGGGGGT 720

TTGACAACCTG GGAAGGCGAT GCGGCTACCG CTTGCGAGGC TTCGCTCGAT CAACAACGGC 780

AATGGATACT CCACATGGCC AAATTGAGCG CTGCGATGGC CAAGCAGGCT CAATATGTCT 840

CGCAGCTGCA CGTGTGGGCT AGGCGGGAAC ATCCGACTTA TGAAGACATA GTCGGGCTCG 900

AACGGCTTTA CGCGGAAAAC CCTTCGGCCC GCGACCAAAT TCTCCCGGTG TACGCGGAGT 960

ATCAGCAGAG GTCGGAGAAG GTGCTGACCG AATACAACAA CAAGGCAGCC CTGGAACCGG 1020

TAAACCCGCC GAAGCCTCCC CCCGCCATCA AGATCGACCC GCCCCCGCCT CCGCAAGAGC 1080

AGGGATTGAT CCCTGGCTTC CTGATGCCGC CGTCTGACGG CTCCGGTGTG ACTCCCGGTA 1140

CCGGGATGCC AGCCGCACCG ATGGTTCCGC CTACCGGATC GCCGGGTGGT GGCCTCCCGG 1200

CTGACACGGC GCGCAGCTG ACGTCGGCTG GCGGGAAGC CGCAGCGCTG TCGGGCGACG 1260

TGGCGGTCAA AGCGGCATCG CTCGGTGGCG GTGGAGGCGG CGGGGTGCCG TCGGCGCCGT 1320

TGGGATCCGC GATCGGGGGC GCCGAATCGG TCGGCCCCGC TGGCGCTGGT GACATTGCCG 1380

GCTTAGGCCA GGGAAGGGCC GGCGGCGGCG CCGCGCTGGG CGGCGGTGGC ATGGGAATGC 1440

CGATGGGTGC CGCGCATCAG GGACAAGGGG GCGCCAAGTC CAAGGGTTCT CAGCAGGAAG 1500

ACGAGGCGCT CTACACCGAG GATCGGGCAT GGACCGAGGC CGTCATTGGT AACCGTCGGC 1560

GCCAGGACAG TAAGGAGTCG AAGTGAGCAT GGACGAATTG GACCCGCATG TCGCCCGGGC 1620

GTTGACGCTG GCGGCGCGGT TTCAGTCGGC CCTAGACGGG ACGCTCAATC AGATGAACAA 1680

CGGATCCTTC CGCGCCACCG ACGAAGCCGA GACCGTCGAA GTGACGATCA ATGGGCACCA 1740

GTGGCTCACC GGCCTGCGCA TCGAAGATGG TTTGCTGAAG AAGCTGGGTG CCGAGGCGGT 1800

GGCTCAGCGG GTCAACGAGG CGCTGCACAA TGCGCAGGCC GCGGCGTCCG CGTATAACGA 1860

CGCGGCGGGC GAGCAGCTGA CCGCTGCGTT ATCGGCCATG TCCCGCGCGA TGAACGAAGG 1920

AATGGCCTAA GCCCATTGTT GCGGTGGTAG CGACTACGCA CCGAATGAGC GCCGCAATGC 1980

GGTCATTAG CGCGCCCGAC ACGGCGTGAG TACGCATTGT CAATGTTTTG ACATGGATCG 2040

GCCGGGTTCG GAGGGCGCCA TAGTCCTGGT CGCCAATATT GCCGCAGCTA GCTGGTCTTA 2100

GGTTCGGTTA CGCTGGTTAA TTATGACGTC CGTTACCA 2138

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: amino acid

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(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met	Thr	Gln	Ser	Gln	Thr	Val	Thr	Val	Asp	Gln	Gln	Glu	Ile	Leu	Asn	1	5	10	15
Arg	Ala	Asn	Glu	Val	Glu	Ala	Pro	Met	Ala	Asp	Pro	Pro	Thr	Asp	Val	20	25	30	
Pro	Ile	Thr	Pro	Cys	Glu	Leu	Thr	Ala	Ala	Lys	Asn	Ala	Ala	Gln	Gln	35	40	45	
Leu	Val	Leu	Ser	Ala	Asp	Asn	Met	Arg	Glu	Tyr	Leu	Ala	Ala	Gly	Ala	50	55	60	
Lys	Glu	Arg	Gln	Arg	Leu	Ala	Thr	Ser	Leu	Arg	Asn	Ala	Ala	Lys	Ala	65	70	75	80
Tyr	Gly	Glu	Val	Asp	Glu	Glu	Ala	Ala	Thr	Ala	Leu	Asp	Asn	Asp	Gly	85	90	95	
Glu	Gly	Thr	Val	Gln	Ala	Glu	Ser	Ala	Gly	Ala	Val	Gly	Gly	Asp	Ser	100	105	110	
Ser	Ala	Glu	Leu	Thr	Asp	Thr	Pro	Arg	Val	Ala	Thr	Ala	Gly	Glu	Pro	115	120	125	
Asn	Phe	Met	Asp	Leu	Lys	Glu	Ala	Ala	Arg	Lys	Leu	Glu	Thr	Gly	Asp	130	135	140	
Gln	Gly	Ala	Ser	Leu	Ala	His	Phe	Ala	Asp	Gly	Trp	Asn	Thr	Phe	Asn	145	150	155	160
Leu	Thr	Leu	Gln	Gly	Asp	Val	Lys	Arg	Phe	Arg	Gly	Phe	Asp	Asn	Trp	165	170	175	
Glu	Gly	Asp	Ala	Ala	Thr	Ala	Cys	Glu	Ala	Ser	Leu	Asp	Gln	Gln	Arg	180	185	190	
Gln	Trp	Ile	Leu	His	Met	Ala	Lys	Leu	Ser	Ala	Ala	Met	Ala	Lys	Gln	195	200	205	
Ala	Gln	Tyr	Val	Ala	Gln	Leu	His	Val	Trp	Ala	Arg	Arg	Glu	His	Pro	210	215	220	
Thr	Tyr	Glu	Asp	Ile	Val	Gly	Leu	Glu	Arg	Leu	Tyr	Ala	Glu	Asn	Pro	225	230	235	240
Ser	Ala	Arg	Asp	Gln	Ile	Leu	Pro	Val	Tyr	Ala	Glu	Tyr	Gln	Gln	Arg	245	250	255	
Ser	Glu	Lys	Val	Leu	Thr	Glu	Tyr	Asn	Asn	Lys	Ala	Ala	Leu	Glu	Pro	260	265	270	

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Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro
275 280 285

Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser
290 295 300

Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met
305 310 315 320

Val Pro Pro Thr Gly Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala
325 330 335

Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp
340 345 350

Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Gly Gly Val
355 360 365

Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg
370 375 380

Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly
385 390 395 400

Gly Gly Ala Ala Leu Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala
405 410 415

Ala His Gln Gly Gln Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu
420 425 430

Asp Glu Ala Leu Tyr Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile
435 440 445

Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys
450 455 460

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ala Gly Asn Val Thr Ser Ala Ser Gly Pro His Arg Phe Gly Ala Pro
1 5 10 15

Asp Arg Gly Ser Gln Arg Arg Arg Arg His Pro Ala Ala Ser Thr Ala
20 25 30

Thr Glu Arg Cys Arg Phe Asp Arg His Val Ala Arg Gln Arg Cys Gly
35 40 45

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Phe Pro Pro Ser Arg Arg Gln Leu Arg Arg Arg Val Ser Arg Glu Ala
 50 55 60
 Thr Thr Arg Arg Ser Gly Arg Arg Asn His Arg Cys Gly Trp His Pro
 65 70 75 80
 Gly Thr Gly Ser His Thr Gly Ala Val Arg Arg Arg His Gln Glu Ala
 85 90 95
 Arg Asp Gln Ser Leu Leu Leu Arg Arg Arg Gly Arg Val Asp Leu Asp
 100 105 110
 Gly Gly Gly Arg Leu Arg Arg Val Tyr Arg Phe Gln Gly Cys Leu Val
 115 120 125
 Val Val Phe Gly Gln His Leu Leu Arg Pro Leu Leu Ile Leu Arg Val
 130 135 140
 His Arg Glu Asn Leu Val Ala Gly Arg Arg Val Phe Arg Val Lys Pro
 145 150 155 160
 Phe Glu Pro Asp Tyr Val Phe Ile Ser Arg Met Phe Pro Pro Ser Pro
 165 170 175
 His Val Gln Leu Arg Asp Ile Leu Ser Leu Leu Gly His Arg Ser Ala
 180 185 190
 Gln Phe Gly His Val Glu Tyr Pro Leu Pro Leu Leu Ile Glu Arg Ser
 195 200 205
 Leu Ala Ser Gly Ser Arg Ile Ala Phe Pro Val Val Lys Pro Pro Glu
 210 215 220
 Pro Leu Asp Val Ala Leu Gln Arg Gln Val Glu Ser Val Pro Pro Ile
 225 230 235 240
 Arg Lys Val Arg Glu Arg Cys Ala Leu Val Ala Arg Phe Glu Leu Pro
 245 250 255
 Cys Arg Phe Phe Glu Ile His Glu Val Gly Phe Thr Gly Arg Gly His
 260 265 270
 Pro Arg Arg Ile Gly
 275

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

205220 218480T

Arg Val Ala Ala Ser Phe Ile Asp Trp Leu Asp Ser Pro Asp Ser Pro
 1 5 10 15
 Leu Asp Pro Ser Leu Val Ser Ser Leu Leu Asn Ala Val Ser Cys Gly
 20 25 30
 Ala Glu Ser Ser Ala Ser Ser Ser Ala Arg Ser Gly Asn Gly Ser Arg
 35 40 45
 Trp Thr Ser Met Pro Ser Gly Thr Arg Pro Gly Pro Arg Arg Ala Thr
 50 55 60
 Ser Arg Asp Asp Arg Arg Ser Ala Thr Ser Val Ile Pro Ser Arg Arg
 65 70 75 80
 Ser Val Ala Pro Arg Ala Glu Phe Gly Thr Arg Leu Ala Ser His Arg
 85 90 95
 Ala Ser Pro Ser Asn Ala Cys Pro Val Arg Ile Val Thr Ser Ala Ser
 100 105 110
 Gly Arg Pro Ile Ser Ser Pro Pro Ile Val Arg Ser Arg Ser Cys Val
 115 120 125
 Asp Lys Asn Gly Arg Arg Cys Ala Ser Gly Tyr Arg Arg Leu Asn Arg
 130 135 140
 Ala Arg Ser Ser Ser Ile Ala Ala Arg Cys Arg Thr Ile Gly Thr Phe
 145 150 155 160
 Arg Arg Ser Arg Tyr Ser Ala Ser Met Arg Val Ser Thr Asn Ser Pro
 165 170 175
 His Val Thr His Gly Val Ala Pro Gly Val Thr Arg Arg Ile Gly Gly
 180 185 190

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Gln Glu Arg Pro Gln Met Cys Gln Arg Val Ser Glu Ile Glu Pro Arg
 1 5 10 15
 Thr Gln Phe Phe Asn Arg Cys Ala Leu Pro His Tyr Trp His Phe Pro
 20 25 30
 Ala Val Ala Val Phe Ser Lys His Ala Ser Leu Asp Glu Leu Ala Pro

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35	40	45
Arg Asn Pro Arg Arg Ser Ser Arg Arg Asp Ala Glu Asp Arg Arg Val		
50	55	60
Ile Phe Ala Ala Thr Leu Val Ala Val Asp Pro Pro Leu Arg Gly Ala		
65	70	75 80
Gly Gly Glu Ala Asp Gln Leu Ile Asp Leu Gly Val Cys Arg Arg Gln		
	85	90 95
Ala Gly Arg Val Arg Arg Gly Gln Glu Leu His His Arg His Arg His		
	100	105 110
Gln Gly Ala Ala Pro Asp Leu Arg Arg Arg Arg Arg His Arg Arg Val		
	115	120 125
Gln Gln His Arg Arg Leu Gln Arg Val Arg Gln Leu Arg Arg Tyr Val		
	130	135 140
Gln Thr Ala His His Arg Arg Phe Ala Arg Thr Asp Arg Val Arg His		
	145	150 155 160
His Val Arg Gly Pro Ser Asn His Arg Arg Arg Arg Val Tyr Arg Gly		
	165	170 175
Arg His Ser Gly Ala Gly Gly Cys Pro Ala Gly Gly Ala Gly Ser Val		
	180	185 190
Gly Gly Ser Ala		
	195	

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Val Arg Cys Gly Thr Leu Val Pro Val Pro Met Val Glu Phe Leu Thr		
1	5	10 15
Ser Thr Asn Ala Pro Ser Leu Pro Ser Ala Tyr Ala Glu Val Asp Lys		
	20	25 30
Leu Ile Gly Leu Pro Ala Gly Thr Ala Lys Arg Trp Ile Asn Gly Tyr		
	35	40 45
Glu Arg Gly Gly Lys Asp His Pro Pro Ile Leu Arg Val Thr Pro Gly		
	50	55 60
Ala Thr Pro Trp Val Thr Trp Gly Glu Phe Val Glu Thr Arg Met Leu		

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65		70		75		80
Ala Glu Tyr Arg Asp Arg Arg Lys Val Pro Ile Val Arg Gln Arg Ala	85		90		95	
Ala Ile Glu Glu Leu Arg Ala Arg Phe Asn Leu Arg Tyr Pro Leu Ala	100		105		110	
His Leu Arg Pro Phe Leu Ser Thr His Glu Arg Asp Leu Thr Met Gly	115		120		125	
Gly Glu Glu Ile Gly Leu Pro Asp Ala Glu Val Thr Ile Arg Thr Gly	130		135		140	
Gln Ala Leu Leu Gly Asp Ala Arg Trp Leu Ala Ser Leu Val Pro Asn	145		150		155	160
Ser Ala Arg Gly Ala Thr Leu Arg Arg Leu Gly Ile Thr Asp Val Ala	165		170		175	
Asp Leu Arg Ser Ser Arg Glu Val Ala Arg Arg Gly Pro Gly Arg Val	180		185		190	
Pro Asp Gly Ile Asp Val His Leu Leu Pro Phe Pro Asp Leu Ala Asp	195		200		205	
Asp Asp Ala Asp Asp Ser Ala Pro His Glu Thr Ala Phe Lys Arg Leu	210		215		220	
Leu Thr Asn Asp Gly Ser Asn Gly Glu Ser Gly Glu Ser Ser Gln Ser	225		230		235	240
Ile Asn Asp Ala Ala Thr Arg Tyr Met Thr Asp Glu Tyr Arg Gln Phe	245		250		255	
Pro Thr Arg Asn Gly Ala Gln Arg Ala Leu His Arg Val Val Thr Leu	260		265		270	
Leu Ala Ala Gly Arg Pro Val Leu Thr His Cys Phe Ala Gly Lys Asp	275		280		285	
Arg Thr Gly Phe Val Val Ala Leu Val Leu Glu Ala Val Gly Leu Asp	290		295		300	
Arg Asp Val Ile Val Ala Asp	305		310			

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTCGTGCCGA TTCGGCACGA GCTGAGCAGC CCAAGGGGCC GTTCGGCGAA GTCATCGAGG	60
CATTCGCCGA CGGGCTGGCC GGCAAGGGTA AGCAAATCAA CACCACGCTG AACAGCCTGT	120
CGCAGGCGTT GAACGCCTTG AATGAGGGCC GCGGCGACTT CTTCGCGGTG GTACGCAGCC	180
TGGCGCTATT CGTCAACGCG CTACATCAGG ACGACCAACA GTTCGTGCGG TTGAACAAGA	240
ACCTTGCGGA GTTCACCGAC AGGTTGACCC ACTCCGATGC GGACCTGTCG AACGCCATCC	300
AGCAATTCTGA CAGCTTGCTC GCCGTGCGCG GCCCGTTCTT CGCCAAGAAC CGCGAGGTGC	360
TGACGCATGA CGTCAATAAT CTCGCGACCG TGACCACCAC GTTGCTGCAG CCCGATCCGT	420
TGGATGGGTT GGAGACCGTC CTGCACATCT TCCCGACGCT GGCGGCGAAC ATTAACCAGC	480
TTTACCATCC GACACACGGT GCGTGGTGT CGCTTTCCGC GTTCACGAAT TTCGCCAACC	540
CGATGGAGTT CATCTGCAGC TCGATTTCAGG CGGGTAGCCG GCTCGGTTAT CAAGAGTCGG	600
CCGAACCTCTG TGCGCAGTAT CTGGCGCCAG TCCTCGATGC GATCAAGTTC AACTACTTTC	660
CGTTCGGCCT GAACGTGGCC AGCACC GCCT CGACACTGCC TAAAGAGATC GCGTACTCCG	720
AGCCCCGCTT GCAGCCGCCC AACGGGTACA AGGACACCAC GGTGCCCCGC ATCTGGGTGC	780
CGGATACGCC GTTGTACACAC CGCAACACGC AGCCCGGTTG GGTGGTGGCA CCCGGGATGC	840
AAGGGGTTC GGTGGGACCG ATCAGCGAGG GTTTGCTGAC GCCGGAGTCC CTGGCCGAAC	900
TCATGGGTGG TCCCGATATC GCCCCCTCCGT CGTCAGGGCT GCAAACCCCG CCCGGACCCC	960
CGAATGCGTA CGACGAGTAC CCCGTGCTGC CGCCGATCGG TTTACAGGCC CCACAGGTGC	1020
CGATACCACC GCCGCCTCCT GGGCCCCGACG TAATCCCGGG TCCGGTGCCA CCGGTCTTGG	1080
CGGCGATCGT GTTCCCAAGA GATCGCCCGG CAGCGTCGGA AAACCTTCGAC TACATGGGCC	1140
TCTTGTTGCT GTCGCCGGGC CTGGCGACCT TCCTGTTCCG GGTGTCATCT AGCCCCGCCC	1200
GTGGAACGAT GGCCGATCGG CACGTGTTGA TACCGGCGAT CACCGGCCTG GCGTTGATCG	1260
CGGCATTCTG CGCACATTCG TGGTACCGCA CAGAACATCC GCTCATAGAC ATGCGCTTGT	1320
TCCAGAACCG AGCGGTCGCG CAGGCCAACA TGACGATGAC GGTGCTCTCC CTCGGGCTGT	1380
TTGGCTCCTT CTTGCTGCTC CCGAGCTACC TCCAGCAAGT GTTGACCAAA TCACCGATGC	1440
AATCGGGGGT GCATATCATC CCACAGGGCC TCGGTGCCAT GCTGGCGATG CCGATCGCCG	1500
GAGCGATGAT GGACCGACCG GGACCGGCCA AGATCGTGCT GGTGGGATC ATGCTGATCG	1560
CTGCGGGGTT GGGCACCTTC GCCTTTGGTG TCGCGCGGCA AGCGGACTAC TTACCCATTC	1620

TGCCGACCGG GCTGGCAATC ATGGGCATGG GCATGGGCTG CTCCATGATG CCACTGTCCG 1680
 GGGCGGCAGT GCAGACCCTG GCCCCACATC AGATCGCTCG CGGTTGACG CTGATCAGCG 1740
 TCAACCAGCA GGTGGGCGGT TCGATAGGGA CCGCACTGAT GTCGGTGCTG CTCACCTACC 1800
 AGTTCAATCA CAGCGAAATC ATCGCTACTG CAAAGAAAGT CGCACTGACC CCAGAGAGTG 1860
 GCGCCGGGCG GGGGGCGGCG GTTGACCCTT CCTCGCTACC GCGCCAAACC AACTTCGCGG 1920
 CCCAACTGCT GCATGACCTT TCGCACGCCT ACGCGGTGGT ATTCGTGATA GCGACCGCGC 1980
 TAGTGGTCTC GACGCTGATC CCCGCGGCAT TCCTGCCGAA ACAGCAGGCT AGTCATCGAA 2040
 GAGCACCGTT GCTATCCGCA TGACGTCTGC TT 2072

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCACCCCGGA GAAGTCGTTC GTCGACGACC TGGACATCGA CTCGCTGTCTG ATGGTCGAGA 60
 TCGCCGTGCA GACCGAGGAC AAGTACGGCG TCAAGATCCC CGACGAGGAC CTCGCCGGTC 120
 TCGGTACCGT CGGTGACGTT GTCGCCTACA TCCAGAAGCT CGAGGAAGAA AACCCGGAGG 180
 CGGCTCAGGC GTTGCGCGCG AAGATTGAGT CGGAGAACCC CGATGCGGCA CGAGCAGATC 240
 GGTGCGTTTC ACCCACATCG CAAGCTCGAG ACGCCCGTCG TCCTCTTGCA CGCTCAGCCA 300
 GGTTGGCGTG TCGCCGCCTT CCAGCAAGTG TTCCACCAC ACGAAGGGAC CCTCGCGAAA 360
 GGTGACTGAT CCGCGGACCA CATAGTCGAT GCCACCGTGG CTGACAATTG CGCCGGGTCC 420
 GAGTTGGCGG GGGCCGAATT GCGGCATTGC GTCGAAGGCC AGCGGATCCC GGCGCCCGCC 480
 CGGCGTGGCT GGTGTTTTGG GCCGCCGAT GGCCACGACG AGAACGACGA TGGCGGCGAT 540
 GAACAGCGCC ACGGCAATCA CGACCAGCAG ATTTCCACG CATAACCTCT CGTACCGCTG 600
 CGCCGCGGTT GGTGATCGG TCGCATATCG ATGGCGCCGT TTAACGTAAC AGCTTTCGCG 660
 GGACCGGGGG TCACAACGGG CGAGTTGTCC GGCCGGGAAC CCGGCAGGTC TCGGCCGCGG 720
 TCACCCAGC TCACTGGTGC ACCATCCGGG TGTCGGTGAG CGTGCAACTC AAACACACTC 780
 AACGGCAACG GTTCTCAGG TCACCAGCTC AACCTCGACC CGCAATCGCT CGTACGTTTC 840

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GACCGCGCGC AGGTCGCGAG TCAGCAGCTT TGCGCCGGCA GCTTTCGCCG TGAAGCCGAC 900
 CAGGGCATCG TAGGTTGCGC CACCGGTGAC ATCGTGCTCG GCGAGGTGGT CCGTCAAGCC 960
 GCGATATGAG CAGGCATCCA GTGCCAGGTA GTTGCTGGAG GTGATGTCCG CCAAGTAGGC 1020
 GTGGACGGCA ACAGGGGCAA TACGATGCGG CCGTGGTAGC CGGGTCAAGA CCGAATAGGT 1080
 TTCCACAGCC GCGTGCGCGA TCAGATGGAC GCCACGGTTG AGCGCGCGCA CGGCGGCCTC 1140
 GTGCCCTTCG TGCCAGGTCG CGAATCCGGC AACCAGCACG CTGGTGTCTG GTGCGATCAC 1200
 CGCCGTGTGC GATCGAGCGT TTCCCGAACG ATTTCTGTCG TCAACGGGGG CAGGGGACGT 1260
 TCTGGCCGTG CGACGAGAAC CGAGCCTTCC CGAACGAGTT CGACACCGGT CGGGGCCGGC 1320
 TCAATCTCGA TGCGCCCATC GCGCTCGGTG ATCTCCACCT GGTCGTTCCC GCGCAAGCCA 1380
 AGGCGCTCGC GAATCCGCTT GGGAATCACC AGACGTCCTG CGACATCGAT GGTGTGTCGC 1440
 ATGGTAGGAA ATTTACCATC GCACGTTCCA TAGGCGTGTC CTGCGCGGGA TGTCGGGACG 1500
 ATCCGCTAGC GTATCGAACG ATTGTTTCGG AAATGGCTGA GGGAGCGTGC GGTGCGGGTG 1560
 ATGGGTGTCG ATCCCGGGTT GACCCGATGC GGGCTGTGCG TCATCGAGAG TGGGCGTGGT 1620
 CGGCAGCTCA CCGCGCTGGA TGTCGACGTG GTGCGCACAC CGTCGGATGC GGCCTTGGCG 1680
 CAGCGCCTGT TGGCCATCAG CGATGCCGTC GAGCACTGGC TGGACACCCA TCATCCGGAG 1740
 GTGGTGGCTA TCGAACGGGT GTTCTCTCAG CTCAACGTGA CCACGGTGAT GGGCACCGCG 1800
 CAGGCCGGCG GCGTGATCGC CCTGGCGGCG GCCAAACGTG GTGTGACGCT GCATTTCCAT 1860
 ACCCCCAGCG AGGTCAAGGC GCGGGTCACT GGCAACGGTT CCGCAGACAA GGCTCAGGTC 1920
 ACC 1923

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGGCGTGCC AGTGTACCG GCGATATGAC GTCGGCATTC AATTTTCGCGG CCCC GCCGGA 60
 CCCGTCGCCA CCAATCTGG ACCACCCGGT CCGTCAATTG CCGAAGGTCG CCAAGTGCCT 120
 GCCCAATGTG GTGCTGGGTT TCTTGAACGA AGGCCTGCCG TATCGGGTGC CCTACCCCCA 180
 AACAAACGCCA GTCCAGGAAT CCGGTCCCGC GCGGCCGATT CCCAGCGGCA TCTGCTAGCC 240

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GGGGATGGTT CAGACGTAAC GGTGGCTAG GTCGAAACCC GCGCCAGGGC CGCTGGACGG 300
 GCTCATGGCA GCGAAATTAG AAAACCCGGG ATATTGTCCG CGGATTGTCA TACGATGCTG 360
 AGTGCTTGGT GGTTCGTGTT TAGCCATTGA GTGTGGATGT GTTGAGACCC TGGCCTGGAA 420
 GGGGACAACG TGCTTTTGCC TCTTGGTCCG CCTTTGCCGC CCGACGCGGT GGTGGCGAAA 480
 CGGGCTGAGT CGGGAATGCT CGGCGGGTTG TCGGTTCCGC TCAGCTGGGG AGTGGCTGTG 540
 CCACCCGATG ATTATGACCA CTGGGCGCCT GCGCCGGAGG ACGGCGCCGA TGTCGATGTC 600
 CAGGCGGCCG AAGGGGCGGA CGCAGAGGCC GCGGCCATGG ACGAGTGGGA TGAGTGGCAG 660
 GCGTGGAAAC AGTGGGTGGC GGAGAACGCT GAACCCCGCT TTGAGGTGCC ACGGAGTAGC 720
 AGCAGCGTGA TTCCGCATTC TCCGGCGGCC GGCTAGGAGA GGGGGCGCAG ACTGTCGTTA 780
 TTTGACCACT GATCGGCGGT CTCGGTGTTC CCGCGGCCGG CTATGACAAC AGTCAATGTG 840
 CATGACAAGT TACAGGTATT AGGTCCAGGT TCAACAAGGA GACAGGCAAC ATGGCAACAC 900
 GTTTTATGAC GGATCCGCAC GCGATGCGGG ACATGGCGGG CCGTTTTGAG GTGCACGCCC 960
 AGACGGTGGA GGACGAGGCT CGCCGGATGT GGGCGTCCGC GCAAAACATC TCGGGNGCGG 1020
 GCTGGAGTGG CATGGCCGAG GCGACCTCGC TAGAC 1055

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CCGCCTCGTT GTTGGCATA TCCGCCGCGG CCGCCTCGAC CGCACTGGCC GTGGCGTGTG 60
 TCCGGGCTGA CCACCGGGAT CGCCGAACCA TCCGAGATCA CCTCGCAATG ATCCACCTCG 120
 CGCAGCTGGT CACCCAGCCA CCGGGCGGTG TCGACAGCG CCTGCATCAC CTTGGTATAG 180
 CCGTCGCGCC CCAGCCGCGA GAAGTTGTAG TACTGGCCCA CCACCTGGTT ACCGGGACGG 240
 GAGAAGTTCA GGGTGAAGGT CGGCATGTCG CCGCCGAGGT AGTTGACCCG GAAAACCAGA 300
 TCCTCCGGCA GGTGCTCGGG CCCGCGCCAC ACGACAAACC CGACGCCGGG ATAGGTCAG 359

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs

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- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

AACGGGCCCCG TGGGCACCGC TCCTCTAAGG GCTCTCGTTG GTCGCATGAA GTGCTGGAAG      60
GATGCATCTT  GGCAGATTCC CGCCAGAGCA AAACAGCCGC TAGTCCTAGT CCGAGTCGCC      120
CGCAAAGTTC  CTCGAATAAC TCCGTACCCG GAGCGCCAAA CCGGGTCTCC TTCGCTAAGC      180
TGCGCGAACC  ACTTGAGGTT CCGGGACTCC TTGACGTCCA GACCGATTCTG TTCGAGTGGC      240
TGATCGGTTC  GCCGCGCTGG CGCGAATCCG CCGCCGAGCG GGGTGATGTC AACCCAGTGG      300
GTGGCCTGGA  AGAGGTGCTC TACGAGCTGT CTCCGATCGA GGACTTCTCC      350
  
```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

Glu Gln Pro Lys Gly Pro Phe Gly Glu Val Ile Glu Ala Phe Ala Asp
1           5           10           15
Gly Leu Ala Gly Lys Gly Lys Gln Ile Asn Thr Thr Leu Asn Ser Leu
20          25          30
Ser Gln Ala Leu Asn Ala Leu Asn Glu Gly Arg Gly Asp Phe Phe Ala
35          40          45
Val Val Arg Ser Leu Ala Leu Phe Val Asn Ala Leu His Gln Asp Asp
50          55          60
Gln Gln Phe Val Ala Leu Asn Lys Asn Leu Ala Glu Phe Thr Asp Arg
65          70          75          80
Leu Thr His Ser Asp Ala Asp Leu Ser Asn Ala Ile Gln Gln Phe Asp
85          90          95
Ser Leu Leu Ala Val Ala Arg Pro Phe Phe Ala Lys Asn Arg Glu Val
100         105         110
Leu Thr His Asp Val Asn Asn Leu Ala Thr Val Thr Thr Thr Leu Leu
115         120         125
Gln Pro Asp Pro Leu Asp Gly Leu Glu Thr Val Leu His Ile Phe Pro
130         135         140
  
```

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Thr Leu Ala Ala Asn Ile Asn Gln Leu Tyr His Pro Thr His Gly Gly
 145 150 155 160
 Val Val Ser Leu Ser Ala Phe Thr Asn Phe Ala Asn Pro Met Glu Phe
 165 170 175
 Ile Cys Ser Ser Ile Gln Ala Gly Ser Arg Leu Gly Tyr Gln Glu Ser
 180 185 190
 Ala Glu Leu Cys Ala Gln Tyr Leu Ala Pro Val Leu Asp Ala Ile Lys
 195 200 205
 Phe Asn Tyr Phe Pro Phe Gly Leu Asn Val Ala Ser Thr Ala Ser Thr
 210 215 220
 Leu Pro Lys Glu Ile Ala Tyr Ser Glu Pro Arg Leu Gln Pro Pro Asn
 225 230 235 240
 Gly Tyr Lys Asp Thr Thr Val Pro Gly Ile Trp Val Pro Asp Thr Pro
 245 250 255
 Leu Ser His Arg Asn Thr Gln Pro Gly Trp Val Val Ala Pro Gly Met
 260 265 270
 Gln Gly Val Gln Val Gly Pro Ile Thr Gln Gly Leu Leu Thr Pro Glu
 275 280 285
 Ser Leu Ala Glu Leu Met Gly Gly Pro Asp Ile Ala Pro Pro Ser Ser
 290 295 300
 Gly Leu Gln Thr Pro Pro Gly Pro Pro Asn Ala Tyr Asp Glu Tyr Pro
 305 310 315 320
 Val Leu Pro Pro Ile Gly Leu Gln Ala Pro Gln Val Pro Ile Pro Pro
 325 330 335
 Pro Pro Pro Gly Pro Asp Val Ile Pro Gly Pro Val Pro Pro Val Leu
 340 345 350
 Ala Ala Ile Val Phe Pro Arg Asp Arg Pro Ala Ala Ser Glu Asn Phe
 355 360 365
 Asp Tyr Met Gly Leu Leu Leu Leu Ser Pro Gly Leu Ala Thr Phe Leu
 370 375 380
 Phe Gly Val Ser Ser Ser Pro Ala Arg Gly Thr Met Ala Asp Arg His
 385 390 395 400
 Val Leu Ile Pro Ala Ile Thr Gly Leu Ala Leu Ile Ala Ala Phe Val
 405 410 415
 Ala His Ser Trp Tyr Arg Thr Glu His Pro Leu Ile Asp Met Arg Leu
 420 425 430
 Phe Gln Asn Arg Ala Val Ala Gln Ala Asn Met Thr Met Thr Val Leu

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435	440	445
Ser Leu Gly Leu Phe Gly 450	Ser Phe Leu Leu Leu 455	Pro Ser Tyr Leu Gln 460
Gln Val Leu His Gln Ser 465	Pro Met Gln Ser Gly 470	Val His Ile Ile Pro 475
Gln Gly Leu Gly Ala Met 485	Leu Ala Met Pro Ile 490	Ala Gly Ala Met Met 495
Asp Arg Arg Gly Pro Ala 500	Lys Ile Val Leu Val 505	Gly Ile Met Leu Ile 510
Ala Ala Gly Leu Gly Thr 515	Phe Ala Phe Gly Val 520	Ala Arg Gln Ala Asp 525
Tyr Leu Pro Ile Leu Pro 530	Thr Gly Leu Ala Ile 535	Met Gly Met Gly Met 540
Gly Cys Ser Met Met Pro 545	Leu Ser Gly Ala Ala 550	Val Gln Thr Leu Ala 555
Pro His Gln Ile Ala Arg 565	Gly Ser Thr Leu Ile 570	Ser Val Asn Gln Gln 575
Val Gly Gly Ser Ile Gly 580	Thr Ala Leu Met Ser 585	Val Leu Leu Thr Tyr 590
Gln Phe Asn His Ser Glu 595	Ile Ile Ala Thr Ala 600	Lys Lys Val Ala Leu 605
Thr Pro Glu Ser Gly Ala 610	Gly Arg Gly Ala Ala 615	Val Asp Pro Ser Ser 620
Leu Pro Arg Gln Thr Asn 625	Phe Ala Ala Gln Leu 630	Leu Leu His Asp Leu Ser 635
His Ala Tyr Ala Val Val 645	Phe Val Ile Ala Thr 650	Ala Leu Val Val Ser 655
Thr Leu Ile Pro Ala Ala 660	Phe Leu Pro Lys Gln 665	Gln Gln Ala Ser His Arg 670
Arg Ala Pro Leu Leu Ser 675	Ala	

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser
 1 5 10 15
 Met Val Glu Ile Ala Val Gln Thr Glu Asp Lys Tyr Gly Val Lys Ile
 20 25 30
 Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala
 35 40 45
 Tyr Ile Gln Lys Leu Glu Glu Glu Asn Pro Glu Ala Ala Gln Ala Leu
 50 55 60
 Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg
 65 70 75 80
 Cys Val Ser Pro Thr Ser Gln Ala Arg Asp Ala Arg Arg Pro Leu Ala
 85 90 95
 Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr
 100 105 110
 Thr Arg Arg Asp Pro Arg Glu Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Ala Cys Gln Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg
 1 5 10 15
 Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser
 20 25 30
 Ile Ala Glu Gly Arg Gln Val Arg Ala Gln Cys Gly Ala Gly Phe Leu
 35 40 45
 Glu Arg Arg Pro Ala Val Ser Gly Ala Leu Pro Pro Asn Asn Ala Ser
 50 55 60
 Pro Gly Ile Arg Ser Arg Ala Ala Asp Ser Gln Arg His Leu Leu Ala
 65 70 75 80
 Gly Asp Gly Ser Asp Val Thr Val Gly
 85

(2) INFORMATION FOR SEQ ID NO:197:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

Ala Ser Leu Leu Ala Tyr Ser Ala Ala Ala Ser Thr Ala Leu Ala
1           5           10           15
Val Ala Cys Val Arg Ala Asp His Arg Asp Arg Arg Thr Ile Arg Asp
          20           25           30
His Leu Ala Met Ile His Leu Ala Gln Leu Val Thr Gln Pro Pro Gly
          35           40           45
Gly Val Arg Gln Arg Leu His His Leu Gly Ile Ala Val Ala Pro Gln
          50           55           60
Pro Gln Glu Val Val Val Leu Ala His His Leu Val Thr Gly Thr Gly
65           70           75           80
Glu Val Gln Gly Glu Gly Arg His Val Ala Ala Glu Val Val Asp Pro
          85           90           95
Glu Asn Gln Ile Leu Arg Gln Val Leu Gly Pro Ala Pro His Asp Lys
          100          105          110
Pro Asp Ala Gly Ile Gly Gln
          115

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(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

```

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu
1           5           10           15
Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Gln Ser Lys Thr Ala
          20           25           30
Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val
          35           40           45
Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu
          50           55           60

```

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Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Glu Trp Leu
65 70 75 80

Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val
85 90 95

Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile
100 105 110

Glu Asp Phe Ser
115

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TGCTACGCAG CAATCGCTTT GGTGACAGAT GTGGATGCCG GCGTCGCTGC TGGCGATGGC	60
GTGAAAGCCG CCGACGTGTT CGCCGCATTC GGGGAGAACA TCGAACTGCT CAAAAGGCTG	120
GTGCGGGCCG CCATCGATCG GGTCGCCGAC GAGCGCACGT GCACGCACTG TCAACACCAC	180
GCCGGTGTTT CGTTGCCGTT CGAGCTGCCA TGAGGGTGCT GCTGACCGGC GCGGCCGGCT	240
TCATCGGGTC GCGCGTGGAT GCGGCGTTAC GGGCTGCGGG TCACGACGTG GTGGGCGTCG	300
ACGCGCTGCT GCCCGCCGCG CACGGGCCAA ACCCGGTGCT GCCACCGGGC TGCCAGCGGG	360
TCGACGTGCG CGACGCCAGC GCGCTGGCCC CGTTGTTGGC CGGTGTGCGT CTGGTGTGTC	420
ACCAGGCCGC CATGGTGGGT GCCGGCGTCA ACGCCGCCGA CGCACCCGCC TATGGCGGCC	480
ACAACGATTT CGCCACCACG GTGCTGCTGG CGCAGATGTT CGCCGCCGGG GTCCGCCGTT	540
TGGTGCTGGC GTCGTCGATG GTGGTTTACG GGCAGGGGCG CTATGACTGT CCCCAGCATG	600
GACCGGTCGA CCCGCTGCCG CGGCGGCGAG CCGACCTGGA CAATGGGGTC TTCGAGCACC	660
GTTGCCCCGGG GTGCGGCGAG CCAGTCATCT GGCAATTGGT CGACGAAGAT GCCCCGTTGC	720
GCCCCGCGCAG CCTGTACGCG GCAGCAAGAC CGCGCAGGAG CACTACGCGC TGGCGTGGTC	780
GGAAACGAAT GGCGGTTCCG TGGTGCGGTT G	811

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GTCCCGCGAT GTGGCCGAGC ATGACTTTCG GCAACACCGG CGTAGTAGTC GAAGATATCG	60
GACTTTGTGG TCCCGGTGGC GGGATAGAGC ACCTGTCGGC GTTGGTCAGC GTCACCCGTT	120
GCTCGGACGC CGAACCCATG CTTTCAACGT AGCCTGTCGG TCACACAAGT CGCGAGCGTA	180
ACGTCACGGT CAAATATCGC GTGGAATTC GCCGTGACGT TCCGCTCGCG GACAATCAAG	240
GCATACTCAC TTACATGCGA GCCATTTGGA CGGGTTCGAT CGCCTTCGGG CTGGTGAACG	300
TGCCGGTCAA GGTGTACAGC GCTACCGCAG ACCACGACAT CAGGTTCCAC CAGGTGCACG	360
CCAAGGACAA CGGACGCATC CGGTACAAGC GCGTCTGCGA GCGTGTGGC GAGGTGGTCG	420
ACTACCGCGA TCTTGCCCGG GCCTACGAGT CCGGCGACGG CCAAATGGTG GCGATCACCG	480
ACGACGACAT CGCCAGCTTG CCTGAAGAAC GCAGCCGGGA GATCGAGGTG TTGGAGTTCG	540
TCCCGCCGCG CGACGTGGAC CCGATGATGT TCGACCGCAG CTACTTTTTG GAGCCTGATT	600
CGAAGTCGTC GAAATCGTAT GTGCTGCTGG CTAAGACACT CGCCGAGACC GACCGGATGG	660
CGATCGTGGA TCGCCCCACC GGCCGTGAAT GCAGGAAAAA TAAGAGCCGC TATCCACAAT	720
TCGGCGTCGA GCTCGGCTAC CACAAACGGT AGAACGATCG AGACATTCCC GAGCTGAAGT	780
GCGGCGCTAT AGAAGCCGCT CTGCGCGATT ATCAAACGCA AAATACGCTT ACTCATGCCA	840
TCGGCGCTGC TCACCCGATG CGACGTTTTT GCCACGCTCC ACCGCCTGCC GCGCGACCTC	900
AAGTGGGCAT GCATCCCACC CGTTCCCGGA AACCGGTTCC GGCGGGTCGG CTCATCGCTT	960
CATCCT	966

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CCGCACCGCC GGCAATACCG CCAGCGCCAC CGTTACCGCC GTTTGCGCCG TTGCCCCCGT	60
TGCCGCCCCGT CCCGCCGGCC CCGCCGATGG AGTTCTCATC GCCAAAAGTA CTGGCGTTGC	120
CACCGGAGCC GCCGTTGCCG CCGTCACCGC CAGCCCCGCC GACTCCACCG GCCCCACCGA	180

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CTCCGCCGCT	GCCACCGTTG	CCGCCGTTGC	CGATCAACAT	GCCGCTGGCG	CCACCCTTGC	240
CACCCACGCC	ACCGGCTCCG	CCCACCCCGC	CGACACCAAG	CGAGCTGCCG	CCGGAGCCAC	300
CATCACCACC	TACGCCACCG	ACCGCCCAGA	CACCAGCGAC	CGGGTCTTCG	TGAAACGTCG	360
CGGTGCCACC	ACCGCCGCCG	TTACCGCCAA	CCCCACCGGC	AACGCCGGCG	CCGCCATCCC	420
CGCCGGCCCC	GGCGTTGCCG	CCGTTGCCGC	CGTTGCCGAA	CAACAACCCG	CCGGCGCCGC	480
CGTTGCCGCC	CGCGCCGCCG	GTCCCGCCGG	CGCCGCCGAC	GCCAAGGCCG	CTGCCGCCCT	540
TGCCGCCATC	ACCACCCTTG	CCGCCGACCA	CATCGGGTTC	TGCCTCGGGG	TCTGGGCTGT	600
CAAACCTCGC	GATGCCAGCG	TTGCCGCCGC	TTCCCCCGGG	CCCCCCCGTG	GCGCCGTCAC	660
CACCGATACC	ACCCGCGCCA	CCGGCGCCAC	CGTTGCCGCC	ATCACCGAAT	AGCAACCCGC	720
CGGCGCCACC	ATTGCCGCCA	GCTCCCCCTG	CGCCACCGTC	GGCGCCGGAG	GCGGCACTGG	780
CAGCCCCGTT	ACCACCGAAA	CCGCCGCTAC	CACCGGTAGA	GGTGGCAGTG	GCGATGTGTA	840
CGAAAGCGCC	GCCTCCGGCG	CCGCCGCTAC	CACCCCCACT	GCCGGCGGCT	ACACCGTCGG	900
ACCCGTTGCC	ACCATCACCG	CCAAAGGCGC	TCGCAATGTC	GCCCTGCGCG	ACTCCGCCGT	960
CGCCGCCGTT	GCCGCCGCCG	CCACCGGCAG	CGGCGGTACC	GCCGTCACCA	CCGGCACCGC	1020
CGGTGGCCTT	GCCCGAGCCT	GCCGTCGCGG	TGGCACCGTC	GCCGCCGGTG	CCACCGGTCG	1080
GCGTGCCGGC	AGTGCCATGG	CCGCCCGTGC	CGCCGTCGCC	GCCGGTTTGA	TCACCGATGC	1140
CGGACACATC	TGCCGGGCTG	TCCCCGGTGC	TGGCCGCGGG	GCCGGGCGTG	GGATTGACCC	1200
CGTTTGCCCC	GGCGAGGCCG	GCGCCGCCGG	TACCACCGGC	GCCGCCATGG	CCGAACAGCC	1260
CGGCGTTGCC	GCCGTTACCG	CCCGCACCCC	CGATGCCTGC	GGCCACGCTG	GTGCCGCCGA	1320
CACCGCCGTT	GCCGCCGTTG	CCCCACAACC	ACCCCCCGTT	CCCACCGGCA	CCGCCGGCCG	1380
CGCCGGTACC	ACCGGCCCCG	CCGTTGCCGC	CGTTGCCGAT	CAACCCGGCC	GCGCCTCCGC	1440
TGCCGCCGGT	TTGACCGAAC	CCGCCAGCCG	CGCCGTTGCC	ACCGTTGCCA	AACAGCAACC	1500
CGCCGGCCGC	GCCAGGCTGC	CCGGGTGCCG	TCCCGTCGGC	GCCGTTTCCG	ATCAACGGGC	1560
GCCCCAAAAG	CGCCTCGGTG	GGCGCATTCA	CCGCACCCAG	CAGACTCCGC	TCAACAGCGG	1620
CTTCAGTGCT	GGCATAACGA	CCCGCGGCCG	CAGTCAACGC	CTGCACAAAC	TGCTCGTGAA	1680
ACGCTGCCAC	CTGTACGCTG	AGCGCCTGAT	ACTGCCGAGC	ATGGGCCCCG	AACAACCCCG	1740
CAATCGCCGC	CGACACTTCA	TCGGCAGCCG	CAGCCACCAC	TTCCGTCGTC	GGGATCGCCG	1800
CGGCCGCATT	AGCCGCGCTC	ACCTGCGAAC	CAATAGTCGA	TAAATCCAAA	GCCGCAGTTG	1860

CCAGCAGCTG CGGCGTCGCG ATCACCAAGG ACACCTCGCA CCTCCGGATA CCCCATATCG 1920
 CCGCACCGTG TCCCCAGCGG CCACGTGACC TTTGGTCGCT GGCTGGCGGC CCTGACTATG 1980
 GCCGCGACGG CCCTCGTTCT GATTCGCCCC GGCGCGCAGC TTGTTGCGCG AGTTGAAGAC 2040
 GGGAGGACAG GCCGAGCTTG GTGTAGACGT GGGTCAAGTG GGAATGCACG GTCCGCGGCG 2100
 AGATGAATAG GCGGACGCCG ATCTCCTTGT TGCTGAGTCC CTCACCGACC AGTAGAGCCA 2160
 CCTCAAGCTC TGTCGGTGTC AACGCGCCCC AGCCACTTGT CGGGCGTTTC CGTGCACCGC 2220
 GGCCTCGTTG CGCGTACGCG ATCGCCTCAT CGATCGATAA CGCAGTTCCT TCGGCCCAGG 2280
 CATEGTEGAA CTEGETGTCA CCCATGGATT TTEGAAGGGT GGCTAGEGAC GAGTTACAGC 2340
 CCGCCTGGTA GATCCCGAAG CGGACCG 2367

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Pro Ala Gly Ala Thr Ile Ala Ala Ser Ser Pro Cys Ala Thr Val
 1 5 10 15
 Gly Ala Gly Gly Gly Thr Gly Ser Pro Val Thr Thr Glu Thr Ala Ala
 20 25 30
 Thr Thr Gly Arg Gly Gly Ser Gly Asp Val Tyr Glu Ser Ala Ala Ser
 35 40 45
 Gly Ala Ala Ala Thr Thr Pro Thr Ala Gly Gly Tyr Thr Val Gly Pro
 50 55 60
 Val Ala Thr Ile Thr Ala Lys Gly Ala Arg Asn Val Ala Leu Arg Asp
 65 70 75 80
 Ser Ala Val Ala Ala Val Ala Ala Ala Ala Thr Gly Ser Gly Gly Thr
 85 90 95
 Ala Val Thr Thr Gly Thr Ala Gly Gly Leu Ala Arg Ala Cys Arg Arg
 100 105 110
 Gly Gly Thr Val Ala Ala Gly Ala Thr Gly Arg Arg Ala Gly Ser Ala
 115 120 125
 Met Ala Ala Arg Ala Ala Val Ala Ala Gly Leu Ile Thr Asp Ala Gly
 130 135 140

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His Ile Cys Arg Ala Val Pro Gly Ala Gly Arg Gly Ala Gly Arg Gly
 145 150 155 160
 Ile Asp Pro Val Cys Pro Gly Glu Ala Gly Ala Ala Gly Thr Thr Gly
 165 170 175
 Ala Ala Met Ala Glu Gln Pro Gly Val Ala Ala Val Thr Ala Arg Thr
 180 185 190
 Pro Asp Ala Cys Gly His Ala Gly Ala Ala Asp Thr Ala Val Ala Ala
 195 200 205
 Val Ala Pro Gln Pro Pro Pro Val Pro Thr Gly Thr Ala Gly Arg Ala
 210 215 220
 Gly Thr Thr Gly Pro Ala Val Ala Ala Val Ala Asp Gln Pro Gly Arg
 225 230 235 240
 Ala Ser Ala Ala Ala Gly Leu Thr Glu Pro Ala Ser Arg Ala Val Ala
 245 250 255
 Thr Val Ala Lys Gln Gln Pro Ala Gly Arg Ala Arg Leu Pro Gly Cys
 260 265 270
 Arg Pro Val Gly Ala Val Ser Asp Gln Arg Ala Pro Gln Lys Arg Leu
 275 280 285
 Gly Gly Arg Ile His Arg Thr Gln Gln Thr Pro Leu Asn Ser Gly Phe
 290 295 300
 Ser Ala Gly Ile Pro Thr Arg Gly Arg Ser Gln Arg Leu His Lys Leu
 305 310 315 320
 Leu Val Lys Arg Cys His Leu Tyr Ala Glu Arg Leu Ile Leu Pro Ser
 325 330 335
 Met Gly Pro Glu Gln Pro Arg Asn Arg Arg Arg His Phe Ile Gly Ser
 340 345 350
 Arg Ser His His Phe Arg Arg Arg Asp Arg Arg Gly Arg Ile Ser Arg
 355 360 365
 Ala His Leu Arg Thr Asn Ser Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

205220" E484800T

GGCCAAAACG	CCCCGGCGAT	CGCGGCCACC	GAGGCCGCCT	ACGACCAGAT	GTGGGCCCAG	60
GACGTGGCGG	CGATGTTTGG	CTACCATGCC	GGGGCTTCGG	CGGCCGTCTC	GGCGTTGACA	120
CCGTTTCGGCC	AGGCGCTGCC	GACCGTGGCG	GGCGGCGGTG	CGCTGGTCAG	CGCGGCCCGC	180
GCTCAGGTGA	CCACGCGGGT	CTTCCGCAAC	CTGGGCTTGG	CGAACGTCCG	CGAGGGCAAC	240
GTCCGCAACG	GTAATGTCCG	GAACCTCAAT	CTCGGCTCGG	CCAACATCGG	CAACGGCAAC	300
ATCGGCAGCG	GCAACATCGG	CAGCTCCAAC	ATCGGGTTTG	GCAACGTGGG	TCCTGGGTTG	360
ACCGCAGCGC	TGAACAACAT	CGGTTTCGGC	AACACCGGCA	GCAACAACAT	CGGGTTTGGC	420
AACACCGGCA	GCAACAACAT	CGGGTTTCGGC	AATACCGGAG	ACGGCAACCG	AGGTATCGGG	480
CTCACGGGTA	GCGGTTTGTT	GGGGTTTCGGC	GGCCTGAACT	CGGGCACCGG	CAACATCGGT	540
CTGTTCAACT	CGGGCACCGG	AAACGTCGGC	ATCGGCAACT	CGGGTACCGG	GAACCTGGGGC	600
ATTGGCAACT	CGGGCAACAG	CTACAACACC	GGTTTTGGCA	ACTCCGGCGA	CGCCAACACG	660
GGCTTCTTCA	ACTCCGGAAT	AGCCAACACC	GGCGTCGGCA	ACGCCGGCAA	CTACAACACC	720
GGTAGCTACA	ACCCGGGCAA	CAGCAATACC	GGCGGCTTCA	ACATGGGCCA	GTACAACACG	780
GGCTACCTGA	ACAGCGGCAA	CTACAACACC	GGCTTGGCAA	ACTCCGGCAA	TGTCAACACC	840
GGCGCCTTCA	TTACTGGCAA	CTTCAACAAC	GGCTTCTTGT	GGCGCGGCGA	CCACCAAGGC	900
CTGATTTTCG	GGAGCCCCGG	CTTCTTCAAC	TCGACCAGTG	CGCCGTCGTC	GGGATTCTTC	960
AACAGCGGTG	CCGGTAGCGC	GTCCGGCTTC	CTGAACTCCG	GTGCCAACAA	TTCTGGCTTC	1020
TTCAACTCTT	CGTCGGGGGC	CATCGGTAAC	TCCGGCCTGG	CAAACGCGGG	CGTGCTGGTA	1080
TCGGGCGTGA	TCAACTCGGG	CAACACCGTA	TCGGGTTTGT	TCAACATGAG	CCTGGTGGCC	1140
ATCACAACGC	CGGCCTTGAT	CTCGGGCTTC	TTCAACACCG	GAAGCAACAT	GTCGGGATTT	1200
TTCGGTGGCC	CACCGGTCTT	CAATCTCGGC	CTGGCAAACC	GGGGCGTCGT	GAACATTCTC	1260
GGCAACGCCA	ACATCGGCAA	TTACAACATT	CTCGGCAGCG	GAAACGTCCG	TGACTTCAAC	1320
ATCCTTGGCA	GCGGCAACCT	CGGCAGCCAA	AACATCTTGG	GCAGCGGCAA	CGTCGGCAGC	1380
TTCAATATCG	GCAGTGGAAG	CATCGGAGTA	TTCAATGTCT	GTTCCGGAAG	CCTGGGAAAC	1440
TACAACATCG	GATCCGGAAA	CCTCGGGATC	TACAACATCG	GTTTTGGAAG	CGTCGGCGAC	1500
TACAACGTCG	GCTTCGGGAA	CGCGGGCGAC	TTCAACCAAG	GCTTTGCCAA	CACCGGCAAC	1560
AACAACATCG	GGTTCGCCAA	CACCGGCAAC	AACAACATCG	GCATCGGGCT	GTCCGGCGAC	1620

AACCAGCAGG GCTTCAATAT TGCTAGCGGC TGGAAGTCGG GCACCGGCAA CAGCGGCCTG 1680
 TTCAATTCGG GCACCAATAA CGTTGGCATC TTCAACGCGG GCACCGGAAA CGTCGGCATC 1740
 GCAAAGTCGG GCACCGGGAA CTGGGGTATC GGGAACCCGG GTACCGACAA TACCGGCATC 1800
 CTCAATGCTG GCAGCTACAA CACGGGCATC CTCAACGCCG GCGACTTCAA CACGGGCTTC 1860
 TACAACACGG GCAGCTACAA CACCGGCGGC TTCAACGTCG GTAACACCAA CACCGGCAAC 1920
 TTCAACGTGG GTGACACCAA TACCGGCAGC TATAACCCGG GTGACACCAA CACCGGCTTC 1980
 TTCAATCCCG GCAACGTCAA TACCGGCGCT TTCGACACGG GCGACTTCAA CAATGGCTTC 2040
 TTGGTGGCGG GCGATAACCA GGGCCAGATT GCCATCGATC TCTCGGTCAC CACTCCATTC 2100
 ATCCCCATAA ACGAGCAGAT GGTCATTGAC GTACACAACG TAATGACCTT CGGCGGCAAC 2160
 ATGATCACGG TCACCGAGGC CTCGACCGTT TTCCCCAAA CCTTCTATCT GAGCGGTTTG 2220
 TTCTTCTTCG GCCCGGTCAA TCTCAGCGCA TCCACGCTGA CCGTTCCGAC GATCACCTC 2280
 ACCATCGGCG GACCGACGGT GACCGTCCCC ATCAGCATTG TCGGTGCTCT GGAGAGCCGC 2340
 ACGATTACCT TCCTCAAGAT CGATCCGGCG CCGGGCATCG GAAATTCGAC CACCAACCCC 2400
 TCGTCCGGCT TCTTCAACTC GGGCACCGGT GGCACATCTG GCTTCCAAAA CGTCGGCGGC 2460
 GGCAGTTCAG GCGTCTGGAA CAGTGGTTTG AGCAGCGCGA TAGGGAATTC GGGTTTCCAG 2520
 AACCTCGGCT CGCTGCAGTC AGGCTGGGCG AACCTGGGCA ACTCCGTATC GGGCTTTTTC 2580
 AACACCAGTA CCGTGAACCT CTCCACGCCG GCCAATGTCT CGGGCCTGAA CAACATCGGC 2640
 ACCAACCTGT CCGGCGTGTT CCGCGGTCCG ACCGGGACGA TTTTCAACGC GGGCCTTGCC 2700
 AACCTGGGCC AGTTGAACAT CGGCAGCGCC TCGTGCCGAA TTCGGCACGA GTTAGATACG 2760
 GTTTCAACAA TCATATCCGC GTTTTGCGGC AGTGCATCAG ACGAATCGAA CCCGGGAAGC 2820
 GTAAGCGAAT AAACCGAATG GCGGCCTGTC AT 2852

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly Gln Asn Ala Pro Ala Ile Ala Ala Thr Glu Ala Ala Tyr Asp Gln
 1 5 10 15

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Met Trp Ala Gln Asp Val Ala Ala Met Phe Gly Tyr His Ala Gly Ala
 20 25 30
 Ser Ala Ala Val Ser Ala Leu Thr Pro Phe Gly Gln Ala Leu Pro Thr
 35 40 45
 Val Ala Gly Gly Gly Ala Leu Val Ser Ala Ala Ala Gln Val Thr
 50 55 60
 Thr Arg Val Phe Arg Asn Leu Gly Leu Ala Asn Val Arg Glu Gly Asn
 65 70 75 80
 Val Arg Asn Gly Asn Val Arg Asn Phe Asn Leu Gly Ser Ala Asn Ile
 85 90 95
 Gly Asn Gly Asn Ile Gly Ser Gly Asn Ile Gly Ser Ser Asn Ile Gly
 100 105 110
 Phe Gly Asn Val Gly Pro Gly Leu Thr Ala Ala Leu Asn Asn Ile Gly
 115 120 125
 Phe Gly Asn Thr Gly Ser Asn Asn Ile Gly Phe Gly Asn Thr Gly Ser
 130 135 140
 Asn Asn Ile Gly Phe Gly Asn Thr Gly Asp Gly Asn Arg Gly Ile Gly
 145 150 155 160
 Leu Thr Gly Ser Gly Leu Leu Gly Phe Gly Gly Leu Asn Ser Gly Thr
 165 170 175
 Gly Asn Ile Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Ile Gly
 180 185 190
 Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn Ser Gly Asn Ser Tyr
 195 200 205
 Asn Thr Gly Phe Gly Asn Ser Gly Asp Ala Asn Thr Gly Phe Phe Asn
 210 215 220
 Ser Gly Ile Ala Asn Thr Gly Val Gly Asn Ala Gly Asn Tyr Asn Thr
 225 230 235 240
 Gly Ser Tyr Asn Pro Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly
 245 250 255
 Gln Tyr Asn Thr Gly Tyr Leu Asn Ser Gly Asn Tyr Asn Thr Gly Leu
 260 265 270
 Ala Asn Ser Gly Asn Val Asn Thr Gly Ala Phe Ile Thr Gly Asn Phe
 275 280 285
 Asn Asn Gly Phe Leu Trp Arg Gly Asp His Gln Gly Leu Ile Phe Gly
 290 295 300
 Ser Pro Gly Phe Phe Asn Ser Thr Ser Ala Pro Ser Ser Gly Phe Phe

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305		310		315		320
Asn Ser Gly Ala Gly Ser Ala Ser Gly Phe Leu Asn Ser Gly Ala Asn						
	325			330		335
Asn Ser Gly Phe Phe Asn Ser Ser Ser Gly Ala Ile Gly Asn Ser Gly						
	340			345		350
Leu Ala Asn Ala Gly Val Leu Val Ser Gly Val Ile Asn Ser Gly Asn						
	355			360		365
Thr Val Ser Gly Leu Phe Asn Met Ser Leu Val Ala Ile Thr Thr Pro						
	370			375		380
Ala Leu Ile Ser Gly Phe Phe Asn Thr Gly Ser Asn Met Ser Gly Phe						
	385			390		395
						400
Phe Gly Gly Pro Pro Val Phe Asn Leu Gly Leu Ala Asn Arg Gly Val						
				405		410
						415
Val Asn Ile Leu Gly Asn Ala Asn Ile Gly Asn Tyr Asn Ile Leu Gly						
				420		425
						430
Ser Gly Asn Val Gly Asp Phe Asn Ile Leu Gly Ser Gly Asn Leu Gly						
				435		440
						445
Ser Gln Asn Ile Leu Gly Ser Gly Asn Val Gly Ser Phe Asn Ile Gly						
				450		455
						460
Ser Gly Asn Ile Gly Val Phe Asn Val Gly Ser Gly Ser Leu Gly Asn						
				465		470
						475
						480
Tyr Asn Ile Gly Ser Gly Asn Leu Gly Ile Tyr Asn Ile Gly Phe Gly						
				485		490
						495
Asn Val Gly Asp Tyr Asn Val Gly Phe Gly Asn Ala Gly Asp Phe Asn						
				500		505
						510
Gln Gly Phe Ala Asn Thr Gly Asn Asn Asn Ile Gly Phe Ala Asn Thr						
				515		520
						525
Gly Asn Asn Asn Ile Gly Ile Gly Leu Ser Gly Asp Asn Gln Gln Gly						
				530		535
						540
Phe Asn Ile Ala Ser Gly Trp Asn Ser Gly Thr Gly Asn Ser Gly Leu						
				545		550
						555
						560
Phe Asn Ser Gly Thr Asn Asn Val Gly Ile Phe Asn Ala Gly Thr Gly						
				565		570
						575
Asn Val Gly Ile Ala Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn						
				580		585
						590
Pro Gly Thr Asp Asn Thr Gly Ile Leu Asn Ala Gly Ser Tyr Asn Thr						
				595		600
						605

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Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly
 610 615 620
 Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn
 625 630 635 640
 Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr
 645 650 655
 Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp
 660 665 670
 Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly
 675 680 685
 Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn
 690 695 700
 Glu Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn
 705 710 715 720
 Met Ile Thr Val Thr Glu Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr
 725 730 735
 Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr
 740 745 750
 Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr
 755 760 765
 Val Pro Ile Ser Ile Val Gly Ala Leu Glu Ser Arg Thr Ile Thr Phe
 770 775 780
 Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro
 785 790 795 800
 Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln
 805 810 815
 Asn Val Gly Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser
 820 825 830
 Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly
 835 840 845
 Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr
 850 855 860
 Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly
 865 870 875 880
 Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn
 885 890 895

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Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys
 900 905 910

Arg Ile Arg His Glu Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe
 915 920 925

Cys Gly Ser Ala Ser Asp Glu Ser Asn Pro Gly Ser Val Ser Glu
 930 935 940

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

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CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGATATCTGC AGAATTCAGG TTAAAGCCC ATTTGCGA

38

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCGCATGCGA GCCACGTGCC CACAACGGCC

30

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTTCATGGAA TTCTCAGGCC GGTAAGGTCC GCTGCGG

37

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7676 base pairs
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG TGGTTACGCG	60
CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC	120
CTTTCTCGCC ACGTTCGCCG GCTTTCCCCG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG	180
GTTCCGATTT AGTGCTTTAC GGCACCTCGA CCCCAGAAAA CTTGATTAGG GTGATGGTTC	240
ACGTAGTGGG CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT	300
CTTTAATAGT GGACTCTTGT TCCAAACTGG AACAACACTC AACCCCTATCT CGGTCTATTC	360
TTTTGATTTA TAAGGGATTT TGCCGATTTT GGCCTATTGG TTAAAAAATG AGCTGATTTA	420
ACAAAAATTT AACGCGAATT TTAACAAAAT ATTAACGTTT ACAATTTTCA GTGGCACTTT	480
TCGGGGAAAT GTGCGCGGAA CCCCTATTTG TTTATTTTTC TAAATACATT CAAATATGTA	540
TCCGCTCATG AATTAATTCT TAGAAAAACT CATCGAGCAT CAAATGAAAC TGCAATTTAT	600
TCATATCAGG ATTATCAATA CCATATTTTT GAAAAAGCCG TTTCTGTAAT GAAGGAGAAA	660
ACTCACCGAG GCAGTTCCAT AGGATGGCAA GATCCTGGTA TCGGTCTGCG ATTCCGACTC	720
GTCCAACATC AATACAACCT ATTAATTTCC CCTCGTCAAA AATAAGGTTA TCAAGTGAGA	780
AATCACCATG AGTGACGACT GAATCCGGTG AGAATGGCAA AAGTTTATGC ATTTCTTTCC	840
AGACTTGTTT AACAGGCCAG CCATTACGCT CGTCATCAAA ATCACTCGCA TCAACCAAAC	900
CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG TTAAAAGGAC	960
AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAACAC TGCCAGCGCA TCAACAATAT	1020
TTTCACCTGA ATCAGGATAT TCTTCTAATA CCTGGAATGC TGTTTTCCCG GGGATCGCAG	1080
TGGTGAGTAA CCATGCATCA TCAGGAGTAC GGATAAAATG CTTGATGGTC GGAAGAGGCA	1140
TAAATTCCGT CAGCCAGTTT AGTCTGACCA TCTCATCTGT AACATCATTG GCAACGCTAC	1200
CTTTGCCATG TTTCAGAAAC AACTCTGGCG CATCGGGCTT CCCATACAAT CGATAGATTG	1260
TCGCACCTGA TTGCCCGACA TTATCGCGAG CCCATTTATA CCCATATAAA TCAGCATCCA	1320
TGTTGGAATT TAATCGCGGC CTAGAGCAAG ACGTTTCCCG TTGAATATGG CTCATAACAC	1380
CCCTTGATTT ACTGTTTATG TAAGCAGACA GTTTTATTGT TCATGACCAA AATCCCTTAA	1440
CGTGAGTTTT CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA	1500

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GATCCTTTTT	TTCTGCGCGT	AATCTGCTGC	TTGCAAACAA	AAAAACCACC	GCTACCAGCG	1560
GTGGTTTGT	TGCCGGATCA	AGAGCTACCA	ACTCTTTTTC	CGAAGGTAAC	TGGCTTCAGC	1620
AGAGCGCAGA	TACCAAATAC	TGTCCTTCTA	GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	1680
AACTCTGTAG	CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	TGTTACCAGT	GGCTGCTGCC	1740
AGTGGCGATA	AGTCGTGTCT	TACCGGGTTG	GA CTCAAGAC	GATAGTTACC	GGATAAGGCG	1800
CAGCGGTCGG	GCTGAACGGG	GGGTTCGTGC	ACACAGCCCA	GCTTGGAGCG	AACGACCTAC	1860
ACCGAACTGA	GATACCTACA	GCGTGAGCTA	TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	1920
AAGGCGGACA	GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	GAGAGCGCAC	GAGGGAGCTT	1980
CCAGGGGGAA	ACGCCTGGTA	TCTTTATAGT	CCTGTCTGGGT	TTCGCCACCT	CTGACTTGAG	2040
CGTCGATTTT	TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	GGAAAAACGC	CAGCAACGCG	2100
GCCTTTTTTAC	GGTTCCTGGC	CTTTTGCTGG	CCTTTTGCTC	ACATGTTCTT	TCCTGCGTTA	2160
TCCCCTGATT	CTGTGGATAA	CCGTATTACC	GCCTTTGAGT	GAGCTGATAC	CGCTCGCCGC	2220
AGCCGAACGA	CCGAGCGCAG	CGAGTCAGTG	AGCGAGGAAG	CGGAAGAGCG	CCTGATGCGG	2280
TATTTTCTCC	TTACGCATCT	GTGCGGTATT	TCACACCGCA	TATATGGTGC	ACTCTCAGTA	2340
CAATCTGCTC	TGATGCCGCA	TAGTTAAGCC	AGTATACACT	CCGCTATCGC	TACGTGACTG	2400
GGTCATGGCT	GCGCCCCGAC	ACCCGCCAAC	ACCCGCTGAC	GCGCCCTGAC	GGGCTTGTCT	2460
GCTCCCGGCA	TCCGCTTACA	GACAAGCTGT	GACCGTCTCC	GGGAGCTGCA	TGTGTCAGAG	2520
GTTTTTACCG	TCATCACCGA	AACGCGCGAG	GCAGCTGCGG	TAAAGCTCAT	CAGCGTGGTC	2580
GTGAAGCGAT	TCACAGATGT	CTGCCTGTTT	ATCCGCGTCC	AGCTCGTTGA	GTTTCTCCAG	2640
AAGCGTTAAT	GTCTGGCTTC	TGATAAAGCG	GGCCATGTTA	AGGGCGGTTT	TTTCCTGTTT	2700
GGTCACTGAT	GCCTCCGTGT	AAGGGGGATT	TCTGTTTCATG	GGGGTAATGA	TACCGATGAA	2760
ACGAGAGAGG	ATGCTCACGA	TACGGGTAC	TGATGATGAA	CATGCCCGGT	TACTGGAACG	2820
TTGTGAGGGT	AAACA ACTGG	CGGTATGGAT	GCGGCGGGAC	CAGAGAAAAA	TCACTCAGGG	2880
TCAATGCCAG	CGCTTCGTTA	ATACAGATGT	AGGTGTTCCA	CAGGGTAGCC	AGCAGCATCC	2940
TGCGATGCAG	ATCCGGAACA	TAATGGTGCA	GGGCGCTGAC	TTCCGCGTTT	CCAGACTTTA	3000
CGAAACACGG	AAACCGAAGA	CCATT CATGT	TGTTGCTCAG	GTCGCAGACG	TTTTCAGCA	3060
GCAGTCGCTT	CACGTTCGCT	CGCGTATCGG	TGATTCATTC	TGCTAACCAG	TAAGGCAACC	3120
CCGCCAGCCT	AGCCGGGTCC	TCAACGACAG	GAGCACGATC	ATGCGCACCC	GTGGGGCCGC	3180

CATGCCGGCG ATAATGGCCT GCTTCTCGCC GAAACGTTTG GTGGCGGGAC CAGTGACGAA	3240
GGCTTGAGCG AGGGCGTGCA AGATTCCGAA TACCGCAAGC GACAGGCCGA TCATCGTCGC	3300
GCTCCAGCGA AAGCGGTCCT CGCCGAAAAT GACCCAGAGC GCTGCCGGGA CCTGTCCTAC	3360
GAGTTGCATG ATAAAGAAGA CAGTCATAAG TCGGGCGACG ATAGTCATGC CCCGCGCCCA	3420
CCGGAAGGAG CTGACTGGGT TGAAGGCTCT CAAGGGCATC GGTGAGATC CCGGTGCCTA	3480
ATGAGTGAGC TAACTTACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA	3540
CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG GTTTGCGTAT	3600
TGGGCGCCAG GGTGGTTTTT CTTTTACCA GTGAGACGGG CAACAGCTGA TTGCCCTTCA	3660
CCGCCTGGCC CTGAGAGAGT TGCAGCAAGC GGTCCACGCT GGTTTGCCCC AGCAGGCGAA	3720
AATCCTGTTT GATGGTGGTT AACGGCGGGA TATAACATGA GCTGTCTTCG STATCGTCGT	3780
ATCCCACTAC CGAGATATCC GCACCAACGC GCAGCCCGGA CTCGGTAATG GCGCGCATTG	3840
CGCCCAGCGC CATCTGATCG TTGGCAACCA GCATCGCAGT GGGAACGATG CCCTCATTCA	3900
GCATTTGCAT GGTTTGTTGA AAACCGGACA TGGCACTCCA GTCGCCTTCC CGTTCCGCTA	3960
TCGGCTGAAT TTGATTGCGA GTGAGATATT TATGCCAGCC AGCCAGACGC AGACGCGCCG	4020
AGACAGAACT TAATGGGCCC GCTAACAGCG CGATTTGCTG GTGACCCAAT GCGACCAGAT	4080
GCTCCACGCC CAGTCGCGTA CCGTCTTCAT GGGAGAAAAT AATACTGTTG ATGGGTGTCT	4140
GGTCAGAGAC ATCAAGAAAT AACGCCGGA CATTAGTGCA GGCAGCTTCC ACAGCAATGG	4200
CATCCTGGTC ATCCAGCGGA TAGTTAATGA TCAGCCCACT GACGCGTTGC GCGAGAAGAT	4260
TGTGCACCGC CGCTTTACAG GCTTCGACGC CGCTTCGTTT TACCATCGAC ACCACCACGC	4320
TGGCACCCAG TTGATCGGCG CGAGATTTAA TCGCCGCGAC AATTGCGAC GCGCGTGCA	4380
GGGCCAGACT GGAGGTGGCA ACGCCAATCA GCAACGACTG TTTGCCCCGCC AGTTGTTGTG	4440
CCACGCGGTT GGGAATGTAA TTCAGCTCCG CCATCGCCGC TTCCACTTTT TCCCGCGTTT	4500
TCGCAGAAAC GTGGCTGGCC TGGTTCACCA CGCGGGAAAC GGTCTGATAA GAGACACCGG	4560
CATACTCTGC GACATCGTAT AACGTTACTG GTTTCACATT CACCACCCTG AATTGACTCT	4620
CTTCCGGGCG CTATCATGCC ATACCGCGAA AGGTTTTGCG CCATTGATG GTGTCCGGGA	4680
TCTCGACGCT CTCCCTTATG CGACTCCTGC ATTAGGAAGC AGCCAGTAG TAGGTTGAGG	4740
CCGTTGAGCA CCGCCGCCGC AAGGAATGGT GCATGCAAGG AGATGGCGCC CAACAGTCCC	4800

CCGGCCACGG GGCCTGCCAC CATACCCACG CCGAAACAAG CGCTCATGAG CCCGAAGTGG 4860
 CGAGCCCGAT CTTCCCCATC GGTGATGTCG GCGATATAGG CGCCAGCAAC CGCACCTGTG 4920
 GCGCCGGTGA TGCCGGCCAC GATGCGTCCG GCGTAGAGGA TCGAGATCTC GATCCCGCGA 4980
 AATTAATACG ACTCACTATA GGGGAATTGT GAGCGGATAA CAATTCCCCT CTAGAAATAA 5040
 TTTTGTTTAA CTTTAAGAAG GAGATATACA TATGGGCCAT CATCATCATC ATCACGTGAT 5100
 CGACATCATC GGGACCAGCC CCACATCCTG GGAACAGGCG GCGGCGGAGG CGGTCCAGCG 5160
 GGCGCGGGAT AGCGTCGATG ACATCCGCGT CGCTCGGGTC ATTGAGCAGG ACATGGCCGT 5220
 GGACAGCGCC GGCAAGATCA CCTACCGCAT CAAGCTCGAA GTGTCGTTCA AGATGAGGCC 5280
 GGCGCAACCG AGGGGCTCGA AACCACCGAG CGGTTGCGCT GAAACGGGCG CCGGCGCCGG 5340
 TACTGTCGCG ACTACCCCGG CGTCGTCGCC GGTGACGTTG GCGGAGACCG GTAGCACGCT 5400
 GCTCTACCCG CTGTTCAACC TGTGGGGTCC GGCCTTTTAC GAGAGGTATC CGAACGTCAC 5460
 GATCACCGCT CAGGGCACCG GTTCTGGTGC CGGGATCGCG CAGGCCGCCG CCGGGACGGT 5520
 CAACATTGGG GCCTCCGACG CCTATCTGTC GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT 5580
 GATGAACATC GCGCTAGCCA TCTCCGCTCA GCAGGTCAAC TACAACCTGC CCGGAGTGAG 5640
 CGAGCACCTC AAGCTGAACG GAAAAGTCCT GGCGGCCATG TACCAGGGCA CCATCAAAAC 5700
 CTGGGACGAC CCGCAGATCG CTGCGCTCAA CCCC GGCGTG AACCTGCCCC GCACCGCGGT 5760
 AGTTCCGCTG CACCGCTCCG ACGGGTCCGG TGACACCTTC TTGTTACCC AGTACCTGTC 5820
 CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC GCCCCGCTTC GGCACCACCG TCGACTTCCC 5880
 GGCGGTGCCG GGTGCGCTGG GTGAGAACGG CAACGGCGGC ATGGTGACCG GTTGCGCCGA 5940
 GACACCGGGC TCGTGGCCT ATATCGGCAT CAGCTTCCTC GACCAGGCCA GTCAACGGGG 6000
 ACTCGGCGAG GCCCAACTAG GCAATAGCTC TGGCAATTTC TTGTTGCCCC ACGCGCAAAG 6060
 CATTGAGGCC GCGGCGGCTG GCTTCGCATC GAAAACCCCG GCGAACCAGG CGATTTTCGAT 6120
 GATCGACGGG CCCGCCCCCG ACGGCTACCC GATCATCAAC TACGAGTACG CCATCGTCAA 6180
 CAACCGGCAA AAGGACGCCG CCACCGCGCA GACCTTGAGG GCATTTCTGC ACTGGGCGAT 6240
 CACCGACGGC AACAAGGCCT CGTTCCTCGA CCAGGTTTCAT TTCCAGCCGC TGCCGCCCGC 6300
 GGTGGTGAAG TTGTCTGACG CGTTGATCGC GACGATTTCC AGCGCTGAGA TGAAGACCGA 6360
 TGCCGCTACC CTCGCGCAGG AGGCAGGTAA TTTCGAGCGG ATCTCCGGCG ACCTGAAAAC 6420
 CCAGATCGAC CAGGTGGAGT CGACGGCAGG TTCGTTGCAG GGCCAGTGGC GCGGCGCGGC 6480

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GGGGACGGCC GCCCAGGCCG CGGTGGTGCG CTTCCAAGAA GCAGCCAATA AGCAGAAGCA 6540
 GGAACCTCGAC GAGATCTCGA CGAATATTCG TCAGGCCGGC GTCCAATACT CGAGGGCCGA 6600
 CGAGGAGCAG CAGCAGGCGC TGTCTCGCA AATGGGCTTT GTGCCACAA CGGCCGCCTC 6660
 GCCGCCGTCG ACCGCTGCAG CGCCACCCGC ACCGGCGACA CCTGTTGCCC CCCCACCACC 6720
 GGCCGCCGCC AACACGCCGA ATGCCCAGCC GGGCGATCCC AACGCAGCAC CTCCGCCGGC 6780
 GCACCCGAAC GCACCGCCGC CACCTGTCAT TGCCCCAAAC GCACCCCAAC CTGTCCGGAT 6840
 CGACAACCCG GTTGGAGGAT TCAGCTTCGC GCTGCCTGCT GGCTGGGTGG AGTCTGACGC 6900
 CGCCCACTTC GACTAGGGTT CAGCACTCCT CAGCAAAACC ACCGGGGACC CGCCATTTC 6960
 CGGACAGCCG CCGCCGGTGG CCAATGACAC CCGTATCGTG CTCGGCCGGC TAGACCAAAA 7020
 GCTTTACGCC AGCGCCGAAG CCACCGACTC CAAGGCCGCG GCCCGGTTGG GCTCGGACAT 7080
 GGGTGAGTTC TATATGCCCT ACCCGGGCAC CCGGATCAAC CAGGAAACCG TCTCGCTTGA 7140
 CGCCAACGGG GTGTCTGGAA GCGCGTCGTA TTACGAAGTC AAGTTCAGCG ATCCGAGTAA 7200
 GCCGAACGGC CAGATCTGGA CGGGCGTAAT CGGCTCGCCC GCGGCGAACG CACCGGACGC 7260
 CGGGCCCCCT CAGCGCTGGT TTGTGGTATG GCTCGGGACC GCCAACAACC CGGTGGACAA 7320
 GGGCGCGGCC AAGGCGCTGG CCGAATCGAT CCGGCCTTTG GTCGCCCCGC CGCCGGCGCC 7380
 GGCACCGGCT CCTGCAGAGC CCGCTCCGGC GCCGGCGCCG GCCGGGGAAG TCGCTCCTAC 7440
 CCCGACGACA CCGACACCGC AGCGGACCTT ACCGGCCTGA GAATTCTGCA GATATCCATC 7500
 AACTGGCGG CCGCTCGAGC ACCACCACCA CCACCACTGA GATCCGGCTG CTAACAAAGC 7560
 CCGAAAGGAA GCTGAGTTGG CTGCTGCCAC CGCTGAGCAA TAACTAGCAT AACCCCTTGG 7620
 GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA GGAACCTATAT CCGGAT 7676

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser
 1 5 10 15
 Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg

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20					25					30					
Asp	Ser	Val	Asp	Asp	Ile	Arg	Val	Ala	Arg	Val	Ile	Glu	Gln	Asp	Met
	35					40						45			
Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile	Thr	Tyr	Arg	Ile	Lys	Leu	Glu	Val
	50					55					60				
Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln	Pro	Arg	Gly	Ser	Lys	Pro	Pro	Ser
	65					70					75				80
Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro
				85					90					95	
Ala	Ser	Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr
			100					105					110		
Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn
			115				120					125			
Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln
	130					135					140				
Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser
	145					150					155				160
Glu	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala
				165					170					175	
Ile	Ser	Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His
			180					185					190		
Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile
		195					200					205			
Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn
	210					215					220				
Leu	Pro	Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly
	225					230					235				240
Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly
			245						250					255	
Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val
			260					265					270		
Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys
	275						280					285			
Ala	Glu	Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp
	290					295					300				
Gln	Ala	Ser	Gln	Arg	Gly	Leu	Gly	Glu	Ala	Gln	Leu	Gly	Asn	Ser	Ser
	305					310					315				320

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Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
 325 330 335
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
 340 345 350
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
 355 360 365
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
 370 375 380
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
 385 390 395 400
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
 405 410 415
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605

10084843 022602
 205229 04848001

Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GTGGCGGCGC	TGCGGCCGGC	CAGCAGAGCG	ATGTGCATCC	GTTGCGGAAC	CTGATCGCGG	60
TCGACGATGA	GCGCGCCGAA	CGCCGCGACG	ACGAAGAACG	TCAGGAAGCC	GTCCAGCAGC	120
GCGGTCCGCG	CGGTGACGAA	GCTGACCCCG	TCGCAGATCA	GCAGCACCCC	GGCGATGGCG	180
CCGACCAATG	TCGACCGGCT	GATCCGCCGC	ACGATCCGCA	CCACCAGCGC	CACCAGGACC	240
ACACCCAGCA	GGGCGCCGGT	GAACCGCCAG	CCGAATCCGT	TGTGACCGAA	GATGGCCTCC	300

205220" E4848007

CCGATCGCGA TCAGCTGCTT ACCGACCGGC GGGTGAACCA CCAGGCCGTA CCCGGGGTTG	360
TCTTCCACCC CATGGTTGTT CAGCACCTGC CAGGCCTGGC GGTGCGTAAT GCTTCTCGTC	420
GAAGATGGGG GTGCCGGCAT CCGTCACCGA GCCC	454

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TGCAGAAGTA CGGCGGATCC TCGGTGGCCG ACGCCGAACG GATTCGCCGC GTCGCCGAAC	60
GCATCGTCGC CACCAAGAAG CAAGGCAATG ACGTCGTCGT CGTCGTCTCT GCCATGGGGG	120
ATACCACCGA CGACCTGCTG GATCTGGCTC AGCAGGTGTG CCCGGCGCCG CCGCCTCGGG	180
AGCTGGACAT GCTGCTTACC GCCGGTGAAC GCATCTCGAA TGCCTTGGTG GCCATGGCCA	240
TCGAGTCGCT CGGCGCGCAT GCCCGGTCGT TCACCGGTTT GCAGGCCGGG GTGATCACCA	300
CCGGCACCCA CGGCAACGCC AAGATCATCG ACGTCACGCC GGGGCGGCTG CAAACCGCCC	360
TTGAGGAAGG GCGGGTCGTC TTGGTGGCCG GATTCCAAGG GGTCAGCCAG GACACCAAGG	420
ATGTCACGAC GTTGGGCCGC GCGGGCTCGG ACACCACCGC CGTCGCCATG	470

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GGCCGGCGTA CCCGGCCGGG ACAAACAACG ATCGATTGAT ATCGATGAGA GACGGAGGAA	60
TCGTGGCCCT TCCCCAGTTG ACCGACGAGC AGCGCGCGGC CGCGTTGGAG AAGGCTGCTG	120
CCGCACGTCG AGCGCGAGCA GAGCTCAAGG ATCGGCTCAA GCGTGGCGGC ACCAACCTCA	180
CCCAGGTCCT CAAGGACGCG GAGAGCGATG AAGTCTTGGG CAAAATGAAG GTGTCTGCGC	240
TGCTTGAGGC CTTGCCAAAG GTGGGCAAGG TCCAGGCGC	279

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

10084843.022502

ACACGGTCGA	ACTCGACGAG	CCCCTCGTGG	AGGTGTCGAC	CGACAAGGTC	GACACCGAAA	60
TCCCTCGCCG	GCCGCGGGTG	TGCTGACCAA	GATCATCGCC	CAAGAAGATG	ACACGGTCGA	120
GGTCGGCGGC	GAGCTCTCTG	TCATTGGCGA	CGCCCATGAT	GCCGGCGAGG	CCGCGGTCCC	180
GGCACCCAG	AAAGTCTCTG	CCGGCCCAAC	CCGAATCCA			219

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TCGCTGCCGA	CATCGGCGCC	GCGCCCGCCC	CCAAGCCCGC	ACCCAAGCCC	GTCCCCGAGC	60
CAGCGCCGAC	GCCGAAGGCC	GAACCCGCAC	CATCGCCGCC	GGCGGCCCCAG	CCAGCCGGTG	120
CGGCCGAGGG	CGCACCGTAC	GTGACGCCGC	TGGTGCGAAA	GCTGGCGTCG	GAAAACAACA	180
TCGACCTCGC	CGGGGTGACC	GGCACCGGAG	TGGGTGGTCG	CATCCGCAAA	CAGGATGTGC	240
TGGCCGCGGC	TGAACAAAAG	AAGCGGGCGA	AAGCACCGGC	GCCGGCCGCC	CAGGCCGCCG	300
CCGCGCCGGC	CCCGAAAGCG	CCGCCTGAAG	ATCCGATGCC	GC		342

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GGGTCTTGGT	CAGTATCAGC	GCCGACGAGG	ACGCCACGGT	GCCCGTCGGC	GGCGAGTTGG	60
CCCGGATCGG	TGTCGCTGCC	GACATCGGCG	CCGCGCCCGC	CCCCAAGCCC	GCACCCAAGC	120
CCGTCCCCGA	GCCAGCGCCG	ACGCCGAAGG	CCGAACCCGC	ACCATCGCCG	CCGGCGGCCC	180
AGCCAGCCCG	TGCGGCCGAG	GGCGCACCGT	ACGTGACGCC	GCTGGTGCGA	AAGCTGGCGT	240
CGGAAAACAA	CATCGACCTC	GCCGGGGTGA	CCGGCACCGG	AGTGGGTGGT	CGCATCCGCA	300
AACAGGATGT	GCTGGCCGCG	GCTGAACAAA	AGAAGCGGGC	GAAAGCACCG	GCGCCCTGAG	360
CGCTTCATCA	CCCGGTTAAC	CAGCTTGCCC	CAGAAGCCGG	CTTCGACCTC	TTCGCGGGTC	420
TTGGTCCGCT	GCAGGCGGTC	GGCGAGCCAG	TTCAGGTTAG	GCGGCCGAAA	TCTTCCAGTT	480
CGCCAGGAAG	GGCACCCGGA	ACAGGGTCCG	CACCC			515

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

202502 "022502" 10084343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CCGACCCCCAA	GGTGCAGATT	CAACAGGCCA	TTGAGGAAGC	ACAGCGCACC	CACCAAGCGC	60
TGACTCAACA	GGCGGCGCAA	GTGATCGGTA	ACCAGCGTCA	ATTGGAGATG	CGACTCAACC	120
GACAGCTGGC	GGACATCGAA	AAGCTTCAGG	TCAATGTGCG	CCAAGCCCTG	ACGCTGGCCG	180
ACCAGGCCAC	CGCCGCCGGA	GACGCTGCCA	AGGCCACCGA	ATACAACAAC	GCCGCCGAGG	240
CGTTTCGAGC	CCAGCTGGTG	ACCGCCGAGC	AGAGCGTCGA	AGACCTCAAG	ACGCTGCATG	300
ACCAGGCGCT	TAGCGCCGCA	GCTCAGGCCA	AGAAGGCCGT	CGAACGAAAT	GCGATGGTGC	360
TGCAGCAGAA	GATCGCCGAG	CGAACCAAGC	TGCTCAGCCA	GCTCGAGCAG	GCGAAGATGC	420
AGGAGCAGGT	CAGCGCATCG	TTGCGGTCTGA	TGAGTGAGCT	CGCCGCGCCA	GGCAACACGC	480
CGAGCCTCGA	CGAGGTGCGC	GACAAGATCG	AGCGTCGCTA	CGCCAACCGG	ATCGGTTCGG	540
CTGAACCTTG	CGAGAGT					557

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CAGGATAGGT	TTCGACATCC	ACCTGGGTTC	CGCACCCGGT	GCGCGACCGT	GTGATAGGCC	60
AGAGGTGGAC	CTGCGCCGAC	CGACGATCGA	TCGAGGAGTC	AACAGAAATG	GCCTTCTCCG	120
TCCAGATGCC	GGCACTCGGT	GAGAGCGTCA	CCGAGGGGAC	GGTTACCCGC	TGGCTCAAAC	180
AGGAAGGCGA	CACGGTCGAA	CTCGACGAGC	CCCTCGTGGA	GGT		223

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAGAAGTACA	TCTGCCGGTC	GATGTCGGCG	AACCACGGCA	GCCAACCGGC	GCAGTAGCCG	60
ACCAGGACCA	CCGCATAACG	CCAGTCCCGG	CGCACAAACA	TACGCCACCC	CGCGTATGCC	120
AGGACTGGCA	CCGCCAGCCA	CCACATCGCG	GGCGTGCCGA	CCAGCATCTC	GGCCTTGACG	180
CACGACTGTG	CGCCGCAGCC	TGCAACGTCT	TGCTGGTCTGA	TGGCGTACAG	CACCGGCCGC	240
AACGACATGG	GCCAGGTCCA	CGGTTTGGAT	TCCCAAGGGT	GGTAGTTGCC	TGCGGAATTC	300
GTCAGGCCCG	CGTGGAAGTG	GAACGCTTTG	GCGGTGTATT	GCCAGAGCGA	GCGCACGGCG	360
TCGGGCAGCG	GAACAACCGA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	420
GCGGTCTCGG	ACGCGAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCGCGAA	CGGGATCAAC	480
CCCAGCGCAT	ACCCGCTGGG	AAGCACGTCA	CGCCGCACTG	TTCCCAGCCA	CGGTCTTTGC	540
ACTTGGTATG	AACGTCGCGC	CGCCACGTCA	ACGCCAGC			578

(2) INFORMATION FOR SEQ ID NO:224:

205220" 2484800T

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

ACAACGATCG ATTGATATCG ATGAGAGACG GAGGAATCGT GGCCCTTCCC CAGTTGACCG      60
ACGAGCAGCG CGCGGCCGCG TTGGAGAAGG CTGCTGCCGC ACGTCGAGCG CGAGCAGAGC      120
TCAAGGATCG GCTCAAGCGT GGCGGCACCA ACCTCACCCA GGTCTCAAG GACGCGGAGA      180
GCGATGAAGT CTTGGGCAAA ATGAAGGTGT CTGCGCTGCT TGAGGCCTTG CCAAAGGTGG      240
GCAAGGTCAA GGGGCGAGGAG ATCATGACCG AGCTGGAAAT TGCGCCCCAC CCCGCCGCCT      300
TCGTGGCCTC GGTGACCGTC AGCGCAAGGC CCTGCTGGAA AAGTTCGGCT CCGCCTAACC      360
CCGCCGGCCG ACGATGCGGG CCGGAAGGCC TGTGGTGGGC GTACCCCCGC ATACGGGGGA      420
GAAGCGGCCT GACAGGGCCA GTCACAATT CAGGCCGAAC GCCCCGGTGG GGGGGAACCC      480
GCCC

```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```

AGGACTGGCA CCGCCAGCCA CCACATCGCG GGCGTGCCGA CCAGCATCTC GGCCTTGACG      60
CACGACTGTG CGCCGCAGCC TGCAACGTCT TGCTGGTCGA TGGCGTACAG CACCGGCCCG      120
AACGACATGG GCCAGGTCCA CGGTTTGGAT TCCCAAGGGT GGTAGTTGCC TGC GGAATTC      180
GTCAGGCCCG CGTGGAAGTG GAACGCTTTG GCGGTGTAGT GCCAGAGCGA GCGCACGGCG      240
TCGGGCAGCG GAACAACCGA GTTGCGACCG ACCGCTTGAC CGACCGCATG CCGATCGATC      300
GCGGTCTCGG ACGCGAACCA CGGAGCGTAG GTGGCCAGAT AGACCGCGAA CGGGATCAAC      360
CCCAGCGCAT ACCCGCTGGG AAGCACGTCA CGCCGCACTG TCCCCAGCCA CCGTCTTTGC      420
ACTTGGTACT GACGTCGCGC CGCCACGTCG AACGCCAGCG CCATCGCGCC GAAGAACAGC      480
ACGAAGTACA CGCCGACCA CTTGGTGGCG CAAGCCAATC CCAAGCAGCA CCCC GGC      537

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

10084843.022502

Gly Gly Ala Ala Ala Gly Gln Gln Ser Asp Val His Pro Phe Ala Asn
 1 5 10 15
 Leu Ile Ala Val Asp Asp Glu Arg Ala Glu Arg Arg Asp Asp Glu Glu
 20 25 30
 Arg Gln Glu Ala Val Gln Gln Arg Gly Pro Arg Gly Asp Glu Ala Asp
 35 40 45
 Pro Val Ala Asp Gln Gln His Pro Gly Asp Gly Ala Asp Gln Cys Arg
 50 55 60
 Pro Ala Asp Pro Pro His Asp Pro His His Gln Arg His Gln Asp His
 65 70 75 80
 Thr Gln Gln Gly Ala Gly Glu Pro Pro Ala Glu Ser Val Val Thr Glu
 85 90 95
 Asp Gly Leu Pro Asp Arg Asp Gln Leu Leu Thr Asp Arg Arg Val Asn
 100 105 110
 His Gln Ala Val Pro Gly Val Val Phe His Pro Met Val Val Gln His
 115 120 125
 Leu Pro Gly Leu Ala Val Arg
 130 135

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gln Lys Tyr Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg
 1 5 10 15
 Val Ala Glu Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val
 20 25 30
 Val Val Val Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu
 35 40 45
 Ala Gln Gln Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu
 50 55 60
 Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
 65 70 75 80
 Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly
 85 90 95
 Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr
 100 105 110
 Pro Gly Arg Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu Val
 115 120 125
 Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu
 130 135 140
 Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Met
 145 150 155

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Pro Ala Tyr Pro Ala Gly Thr Asn Asn Asp Arg Leu Ile Ser Met Arg
 1           5           10           15
Asp Gly Gly Ile Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Ala
      20           25           30
Ala Ala Leu Glu Lys Ala Ala Ala Arg Arg Ala Arg Ala Glu Leu
      35           40           45
Lys Asp Arg Leu Lys Arg Gly Gly Thr Asn Leu Thr Gln Val Leu Lys
 50           55           60
Asp Ala Glu Ser Asp Glu Val Leu Gly Lys Met Lys Val Ser Ala Leu
65           70           75           80
Leu Glu Ala Leu Pro Lys Val Gly Lys Val Gln Ala
      85           90

```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Thr Val Glu Leu Asp Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val
 1           5           10           15
Asp Thr Glu Ile Pro Ser Pro Ala Ala Gly Val Leu Thr Lys Ile Ile
      20           25           30
Ala Gln Glu Asp Asp Thr Val Glu Val Gly Gly Glu Leu Ser Val Ile
      35           40           45
Gly Asp Ala His Asp Ala Gly Glu Ala Ala Val Pro Ala Pro Gln Lys
 50           55           60
Val Ser Ala Gly Pro Thr Arg Ile
65           70

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Ala Ala Asp Ile Gly Ala Ala Pro Ala Pro Lys Pro Ala Pro Lys Pro
 1           5           10           15
Val Pro Glu Pro Ala Pro Thr Pro Lys Ala Glu Pro Ala Pro Ser Pro
          20           25           30
Pro Ala Ala Gln Pro Ala Gly Ala Ala Glu Gly Ala Pro Tyr Val Thr
          35           40           45
Pro Leu Val Arg Lys Leu Ala Ser Glu Asn Asn Ile Asp Leu Ala Gly
          50           55           60
Val Thr Gly Thr Gly Val Gly Gly Arg Ile Arg Lys Gln Asp Val Leu
65           70           75           80
Ala Ala Ala Glu Gln Lys Lys Arg Ala Lys Ala Pro Ala Pro Ala Ala
          85           90           95
Gln Ala Ala Ala Ala Pro Ala Pro Lys Ala Pro Pro Glu Asp Pro Met
          100          105          110
Pro

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala Thr Val Pro Val Gly
 1           5           10           15
Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Asp Ile Gly Ala Ala Pro
          20           25           30
Ala Pro Lys Pro Ala Pro Lys Pro Val Pro Glu Pro Ala Pro Thr Pro
          35           40           45
Lys Ala Glu Pro Ala Pro Ser Pro Pro Ala Ala Gln Pro Ala Gly Ala
          50           55           60
Ala Glu Gly Ala Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Ser
65           70           75           80
Glu Asn Asn Ile Asp Leu Ala Gly Val Thr Gly Thr Gly Val Gly Gly
          85           90           95
Arg Ile Arg Lys Gln Asp Val Leu Ala Ala Ala Glu Gln Lys Lys Arg
          100          105          110
Ala Lys Ala Pro Ala Pro
          115

```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10084843 " 022502

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Glu Ala Gln Arg Thr
 1           5           10           15
His Gln Ala Leu Thr Gln Gln Ala Ala Gln Val Ile Gly Asn Gln Arg
      20           25           30
Gln Leu Glu Met Arg Leu Asn Arg Gln Leu Ala Asp Ile Glu Lys Leu
      35           40           45
Gln Val Asn Val Arg Gln Ala Leu Thr Leu Ala Asp Gln Ala Thr Ala
      50           55           60
Ala Gly Asp Ala Ala Lys Ala Thr Glu Tyr Asn Asn Ala Ala Glu Ala
65           70           75           80
Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu Asp Leu Lys
      85           90           95
Thr Leu His Asp Gln Ala Leu Ser Ala Ala Gln Ala Lys Lys Ala
      100          105          110
Val Glu Arg Asn Ala Met Val Leu Gln Gln Lys Ile Ala Glu Arg Thr
      115          120          125
Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu Gln Val Ser
      130          135          140
Ala Ser Leu Arg Ser Met Ser Glu Leu Ala Ala Pro Gly Asn Thr Pro
145          150          155          160
Ser Leu Asp Glu Val Arg Asp Lys Ile Glu Arg Arg Tyr Ala Asn Ala
      165          170          175
Ile Gly Ser Ala Glu Leu Ala Glu Ser
      180          185

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Val Ser Thr Ser Thr Trp Val Pro His Pro Val Arg Asp Arg Val Ile
 1           5           10           15
Gly Gln Arg Trp Thr Cys Ala Asp Arg Arg Ser Ile Glu Glu Ser Thr
      20           25           30
Glu Met Ala Phe Ser Val Gln Met Pro Ala Leu Gly Glu Ser Val Thr
      35           40           45
Glu Gly Thr Val Thr Arg Trp Leu Lys Gln Glu Gly Asp Thr Val Glu
      50           55           60
Leu Asp Glu Pro Leu Val Glu
65           70

```

(2) INFORMATION FOR SEQ ID NO:234:

205220" E4848001

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Glu Val His Leu Pro Val Asp Val Gly Glu Pro Arg Gln Pro Thr Gly
 1           5           10           15
Ala Val Ala Asp Gln Asp His Arg Ile Thr Pro Val Pro Ala His Lys
          20           25           30
His Thr Pro Pro Arg Val Cys Gln Asp Trp His Arg Gln Pro Pro His
          35           40           45
Arg Gly Arg Ala Asp Gln His Leu Gly Leu Asp Ala Arg Leu Cys Ala
          50           55           60
Ala Ala Cys Asn Val Leu Leu Val Asp Gly Val Gln His Arg Pro Gln
65           70           75           80
Arg His Gly Pro Gly Pro Arg Phe Gly Phe Pro Arg Val Val Val Ala
          85           90           95
Cys Gly Ile Arg Gln Ala Arg Val Glu Val Glu Arg Phe Gly Gly Val
          100          105          110
Leu Pro Glu Arg Ala His Gly Val Gly Gln Arg Asn Asn Arg Val Ala
          115          120          125
Thr Asp Arg Leu Thr Asp Arg Met Pro Ile Asp Arg Gly Leu Gly Arg
          130          135          140
Glu Pro Arg Ser Val Gly Gly Gln Ile Asp Arg Glu Arg Asp Gln Pro
145          150          155          160
Gln Arg Ile Pro Ala Gly Lys His Val Thr Pro His Cys Ser Gln Pro
          165          170          175
Arg Ser Leu His Leu Val
          180

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Asn Asp Arg Leu Ile Ser Met Arg Asp Gly Gly Ile Val Ala Leu Pro
 1           5           10           15
Gln Leu Thr Asp Glu Gln Arg Ala Ala Leu Glu Lys Ala Ala Ala
          20           25           30
Ala Arg Arg Ala Arg Ala Glu Leu Lys Asp Arg Leu Lys Arg Gly Gly
          35           40           45
Thr Asn Leu Thr Gln Val Leu Lys Asp Ala Glu Ser Asp Glu Val Leu
          50           55           60

```

10084843.022502

Gly Lys Met Lys Val Ser Ala Leu Leu Glu Ala Leu Pro Lys Val Gly
 65 70 75 80
 Lys Val Lys Ala Gln Glu Ile Met Thr Glu Leu Glu Ile Ala Pro His
 85 90 95
 Pro Ala Ala Phe Val Ala Ser Val Thr Val Ser Ala Arg Pro Cys Trp
 100 105 110
 Lys Ser Ser Ala Pro Pro Asn Pro Ala Gly Arg Arg Cys Gly Pro Glu
 115 120 125
 Gly Leu Trp Trp Ala Tyr Pro Arg Ile Arg Gly Arg Ser Gly Leu Thr
 130 135 140
 Gly Pro Ala His Asn Ser Gly Arg Thr Pro Arg Trp Gly Gly Thr Arg
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Asp Trp His Arg Gln Pro Pro His Arg Gly Arg Ala Asp Gln His Leu
 1 5 10 15
 Gly Leu Asp Ala Arg Leu Cys Ala Ala Ala Cys Asn Val Leu Leu Val
 20 25 30
 Asp Gly Val Gln His Arg Pro Gln Arg His Gly Pro Gly Pro Arg Phe
 35 40 45
 Gly Phe Pro Arg Val Val Val Ala Cys Gly Ile Arg Gln Ala Arg Val
 50 55 60
 Glu Val Glu Arg Phe Gly Gly Val Val Pro Glu Arg Ala His Gly Val
 65 70 75 80
 Gly Gln Arg Asn Asn Arg Val Ala Thr Asp Arg Leu Thr Asp Arg Met
 85 90 95
 Pro Ile Asp Arg Gly Leu Gly Arg Glu Pro Arg Ser Val Gly Gly Gln
 100 105 110
 Ile Asp Arg Glu Arg Asp Gln Pro Gln Arg Ile Pro Ala Gly Lys His
 115 120 125
 Val Thr Pro His Cys Pro Gln Pro Arg Ser Leu His Leu Val Leu Thr
 130 135 140
 Ser Arg Arg His Val Glu Arg Gln Arg His Arg Ala Glu Glu Gln His
 145 150 155 160
 Glu Val His Ala Gly Pro Leu Gly Gly Ala Ser Gln Ser Gln Ala Ala
 165 170 175
 Pro Arg

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

ATGCCAAGCC GGTGCTGATG CCCGAGCTCG GCGAATCGGT GACCGAGGGG ACCGTCATTC	60
GTTGGCTGAA GAAGATCGGG GATTCGGTTC AGGTTGACGA GCCACTCGTG GAGGTGTCCA	120
CCGACAAGGT GGACACCGAG ATCCCGTCCC CGGTGGCTGG GGTCTTGGTC AGTATCAGCG	180
CCGACGAGGA CGCCACGGTG CCCGTCGGCG GCGAGTTGGC CCGATCGGT GTCGCTGCCG	240
AGATCGGCGC CGCGCCCGCC CCAAGCCCC C	271

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Ala	Lys	Pro	Val	Leu	Met	Pro	Glu	Leu	Gly	Glu	Ser	Val	Thr	Glu	Gly	
1				5				10						15		
Thr	Val	Ile	Arg	Trp	Leu	Lys	Lys	Ile	Gly	Asp	Ser	Val	Gln	Val	Asp	
			20				25						30			
Glu	Pro	Leu	Val	Glu	Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	Pro	
			35				40					45				
Ser	Pro	Val	Ala	Gly	Val	Leu	Val	Ser	Ile	Ser	Ala	Asp	Glu	Asp	Ala	
			50			55					60					
Thr	Val	Pro	Val	Gly	Gly	Glu	Leu	Ala	Arg	Ile	Gly	Val	Ala	Ala	Glu	
65				70					75				80			
Ile	Gly	Ala	Ala	Pro	Ala	Pro	Lys	Pro								
				85												

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAGGTAGCGG ATGGCCGGAG GAGCACCCCA GGACCGCGCC CGAACCGCGG GTGCCGGTCA	60
TCGATATGTG GGCACCGTTC GTTCCGTCCG CCGAGGTCAT TGACGAT	107

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

ATGAAGTTGA AGTTTGCTCG CCTGAGTACT GCGATACTGG GTTGTGCAGC GGCGCTTGTG      60
TTTCCTGCCT CGGTTGCCAG CGCAGATCCA CCTGACCCGC ATCAGCCGGA CATGACGAAA      120
GGCTATTGCC CGGGTGGCCG ATGGGGTTTT GGCGACTTGG CCGTGTGCGA CGGCGAGAAG      180
TACCCCGACG GCTCGTTTTG GCACCAGTGG ATGCAAACGT GGTTTACCGG CCCACAGTTT      240
TACTTCGATT GTGTCAGCGG CGGTGAGCCC CTCCCCGGCC CGCCGCCACC GGGTGGTTGC      300
GGTGGGGCAA TTCCGTCCGA GCAGCCCAAC GTCCTCTGA      339

```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
 1             5             10             15
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
 20             25             30
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
 35             40             45
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
 50             55             60
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
 65             70             75             80
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
 85             90             95
Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
100             105             110

```

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

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GTGACCACGG	TGGGCCTGCC	ACCAACCCGG	GCAGCGGCAG	CCGCGGCGGC	GCCGGCGGGCT	60
CCGGCGGCAA	CGGTGGCGCC	GGGGGTAACG	CCACCGGCTC	AGGCGGCAAG	GGCGGCGCCG	120
GTGGCAATGG	CGGTGATGGG	AGCTTCGGCG	CTACCAGCGG	CCCCGCCTCC	ATCGGGGTCA	180
CGGGCGCCCC	CGGCGGCAAC	GGCGGCAAGG	GCGGCGCCGG	TGGCAGCAAC	CCCAACGGCT	240
CAGGTGGCGA	CGGCGGCAAA	GGCGGCAACG	GCGGTGCCGG	CGGCAACGGG	GGCTCGATCG	300
GCGCCAACAG	CGGCATCGTC	GGCGGTTCCG	GTGGGGCCGG	TGGCGCTGGC	GGCGCCGGCG	360
GAAACGGCAG	C					371

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GTCCGGGTCC	CACCACCGCG	CCGGCGCGCC	CCTAGCGGCC	GGGCGCACCA	GCCCCTTTTC	60
TTGACTCGTT	CAAGAAAAGG	GCCTTCTGTT	TGGTCGGCCA	TGTTGGCATG	ATCGTGACCC	120
ATGGGCAACA	TCGACGTCGA	CATCTCGGCC	AAGGTCTAGC	TCCATGCGAA	TCGCCGCCGC	180
GGTGGTGAGC	ATCGGTCTAG	CCGTCAATAG	AGGGTTCGCG	GTACCTGTTG	CCGACGCACA	240
CCCGTCGGAG	CCCGGGGTTG	TGTCCTACGC	GGTGCTCGGA	AAGGGGTCGG	TCGGCAACAT	300
CGTCGGCGCC	CCAATGGGGT	GGGAGGCGGT	GTTACCAAG	CCGTTCCAGG	CGTTTTGGGT	360
CGAACTACCG	GCGTGCAACA	ACTGGGTGGA	CATCGGGCTG	CCCGAGGTGT	ACGACGATCC	420
CGAC						424

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GCGATGGCGG	CCGCGGGTAC	CACCGCCAAT	GTGGAACGGT	TTCCCAACCC	CAACGATCCT	60
TTGCATCTGG	CGTCAATTGA	CTTCAGCCCG	GCCGATTTCG	TCACCGAGGG	CCACCGTCTA	120
AGGGCGGATG	CGATCCTACT	GCGCCGTACC	GACCGGCTGC	CTTTCGCCGA	GCCGCCGGAT	180
TGGGACTTGG	TGGAGTCGCA	GTTGCGCACG	ACCGTCACCG	CCGACACGGT	GCGCATCGAC	240
GTCATCGCCG	ACGATATGCG	TCCCGAACTG	GCGGCGGCGT	CCAAACTCAC	CGAATCGCTG	300
CGGCTCTACG	ATTCGTC					317

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TGGCGTATGC	GCTTCGCAGC	CGGTGCCGCG	TCAACGCGCC	GGAGGCAATC	GCTTCGCTGC	60
CGAGGAATGG	TTCGATCACG	ATCGCAGTGT	GCCGTCTGTC	ACCGACACCG	CCGTCCAACG	120
TGAACTGAGG	GCGGAAAATC	GGCCGAAATC	TCGCCCTCAG	TTCACGCTCG	GCGCCTAACG	180
GTTCTGGAAG	TTGGGTGCGC	GCTTCTCGGC	GAACGCGCGC	GGGCCTTCCT	TGGCGTCGTC	240
GGACAGGAAG	ACCTTGATGC	CGATCTGGGT	GTCGATCTTG	AACGCCTCGT	TTTCGGGCAT	300
GCACTCGGTC	TCGCGGATGG	ACCGCAAGAT	GGCCTGCACG	GCCAGGGGTC	CGTTAGCCGA	360
GATGGCGTCG	GCAAGTTCTA	GAACCTTGGT	CAACGCCTGG	CCGTCGGGCA	CACGTGGCCG	420
AT						422

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GCGTGCCGCT	GAACACCAGC	CCGCGGCTGC	CAGATCTCCC	GGACTCGGTA	GTGCCGCCCG	60
TGGCGTCGTT	GCTCTCCTGA	CGGGGCGCGG	CGACCATAAG	GTCGCTAATG	CCCAGGTAGC	120
GGCCCAGGTG	CATGGAGTCG	ATGATGATGC	GACTCTCCAG	CTCGCCGACC	GGGAGCTTGG	180
CATCGGGCCT	GATCAGCCAG	GACGCGTAGG	ACAAGTCGAT	CGAATGCATA	GTGGCCTCCA	240
GAGTGGCCGT	GCCACTTCCG	GCGTGCTCCA	CGGCAAATGC	CTTGATTTCT	AGCTCCGCGT	300
AGTGTTCCCG	CATCGCCTGC	GGGATGAATG	GGAACCGCAG	GATGGCGACA	AACGGGTCTG	360
ACCTCAGGTT	TGCCGCTTTG	CGCACAGTGG	TCGACAGCCG	GTACTCGGCA	TAAATGCTGG	420
CCCCGA						426

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

AGACCGGCCGA	GGGTGTGGTC	GCTGCCCCGCG	GCATTGTCGA	TAATCTGCGC	TGGGTGCGACG	60
CGCCGATCAA	CTAGTGAGGC	GCAACGCTAG	GCTTTGGGAT	ACCCACAGCT	AAAAAGTTTA	120
TCAAAGAAAC	GAAGAAGGTT	GCCATGAGCA	CTGTTGCCGC	CTACGCCGCC	ATGTCGGCGA	180
CCGAACCCCT	GACCAAGACC	ACGATCACCC	GTCGCGACCC	GGGCCCCGAC	GACATGGCGA	240
TCGACATCAA	ATTGCGCGGA	ATCTGTCGCT	CGGACATCCA	TACCGTCCAA	ACCGAATGGG	300
GGCAACCGAA	TTTACCTGTG	GTCCCTG				327

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(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

Asp His Gly Gly Pro Ala Thr Asn Pro Gly Ser Gly Ser Arg Gly Gly
 1           5           10           15
Ala Gly Gly Ser Gly Gly Asn Gly Gly Ala Gly Gly Asn Ala Thr Gly
 20           25           30
Ser Gly Gly Lys Gly Gly Ala Gly Gly Asn Gly Gly Asp Gly Ser Phe
 35           40           45
Gly Ala Thr Ser Gly Pro Ala Ser Ile Gly Val Thr Gly Ala Pro Gly
 50           55           60
Gly Asn Gly Gly Lys Gly Gly Ala Gly Gly Ser Asn Pro Asn Gly Ser
 65           70           75           80
Gly Gly Asp Gly Gly Lys Gly Gly Asn Gly Gly Ala Gly Gly Asn Gly
 85           90           95
Gly Ser Ile Gly Ala Asn Ser Gly Ile Val Gly Gly Ser Gly Gly Ala
 100          105          110
Gly Gly Ala Gly Gly Ala Gly Gly Asn Gly Ser
 115          120

```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

Met Ala Ala Ala Gly Thr Thr Ala Asn Val Glu Arg Phe Pro Asn Pro
 1           5           10           15
Asn Asp Pro Leu His Leu Ala Ser Ile Asp Phe Ser Pro Ala Asp Phe
 20           25           30
Val Thr Glu Gly His Arg Leu Arg Ala Asp Ala Ile Leu Leu Arg Arg
 35           40           45
Thr Asp Arg Leu Pro Phe Ala Glu Pro Pro Asp Trp Asp Leu Val Glu
 50           55           60
Ser Gln Leu Arg Thr Thr Val Thr Ala Asp Thr Val Arg Ile Asp Val
 65           70           75           80
Ile Ala Asp Asp Met Arg Pro Glu Leu Ala Ala Ser Lys Leu Thr
 85           90           95
Glu Ser Leu Arg Leu Tyr Asp Ser
 100

```

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(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Ala Tyr Ala Leu Arg Ser Arg Cys Arg Val Asn Ala Pro Glu Ala Ile
 1 5 10 15
 Ala Ser Leu Pro Arg Asn Gly Ser Ile Thr Ile Ala Val Cys Arg Arg
 20 25 30
 Ala Pro Thr Pro Pro Ser Asn Val Asn
 35 40

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Val Pro Leu Asn Thr Ser Pro Arg Leu Pro Asp Leu Pro Asp Ser Val
 1 5 10 15
 Val Pro Pro Val Ala Ser Leu Leu Ser
 20 25

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Met Ser Thr Val Ala Ala Tyr Ala Ala Met Ser Ala Thr Glu Pro Leu
 1 5 10 15
 Thr Lys Thr Thr Ile Thr Arg Arg Asp Pro Gly Pro His Asp Met Ala
 20 25 30
 Ile Asp Ile Lys Phe Ala Gly Ile Cys Arg Ser Asp Ile His Thr Val
 35 40 45

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Gln Thr Glu Trp Gly Gln Pro Asn Leu Pro Val Val Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GCTTGGAGCC	CTGGAGCGAC	GGTGTGGGTC	TGGGGGTCGA	TTCGTTCTCG	GCGAAAGTCA	60
ACTAAAGACC	ACGTTGACAC	CCAACCGGCG	GCCCGGCATG	GGCCGTCGCG	GCGTAGAAGC	120
TTTGACCGCG	GCGCGAAACG	TTCGCTGCTG	CGGCCCATGC	AGATCGCACA	CGCTTGCTTG	180
AACATCGGGT	GGAGCCGGTG	GTAACGCCAG	GCT			213

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CCGAGCTGCT	GTTCCGGCGCC	GGCGGTGCGG	GCGGCGCGGG	TGGGGCGGGC	ACCGACGGCG	60
GGCCCGGTGC	TACCGGCGGG	ACCGGCGGAC	ACGGCGGAGT	CGGCGGCGAC	GGCGGATGGC	120
TGGCACCCGG	CGGGGCCGCG	GGGGCCGGCG	GGCAAGGCGG	GGCAGGTGGT	GCCCGCAGCG	180
ATGGTGGCGC	GTTGGGTGGT	ACCGGCGGGA	CGGGCGGTAC	CGGCGGCGCC	GGTGGCGCCG	240
GCGGTCGCGG	CACACTGCTG	CTGGGCGCTG	GCGGACAGGG	CGGCCTCGGC	GGCGCCGGCG	300
GACAAGGCGG	CACCGGCGGG	GGCCGGCGGA	GATGGCGTTC	TGGGGGGTGT	CAGTGGCACT	360
GGTGGTA						367

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

AAGGCGTGAT	TGGCAAGGCG	ACCGCGCAGC	GGCCCGTAGC	CGCGGGACGG	CCCAGGCCCC	60
GACCGCAGCG	GCCGGTGTCT	GACCGGGTCA	GCGACCAGCG	GCGCTGACCG	TGCCGCTCGT	120
CTACTTCGAC	GCCAGCGCCT	TCGTCAAAC	TCTCACCACC	GAGACAGGGA	GCTCGCTGGC	180

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GTCCGCTCTA TGGGACGGCT GCGACGCCGC ATTGTCCAAC CGCCTGGCCT ACCCCGAAGT 240
 CCGCGCCGCA CTCGCTGCAA CGGGCCGCAA TCACGACCTA ACCGAATCCG AGCTCGCCGA 300
 CGCCGAGCGT GACTGGGAGG ACTTCTGGGC CGCACCCGCC CAGTCGAACT CACCGCGACG 360
 GTTGAACAGC ACGCCGGGCA CCTCGCCCCG ACACATGCCT TACGCGGAGC CGACACCGTT 420

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

CTCTTGTCGG TGGCATCGGC GGTACCGGCG GAACCGGCGG CAACGCCGGT ATGCTCGCCG 60
 GCGCCGCCGG GGCCGGCGGT GCCGGCGGGT TCAGCTTCAG CACTGCCGGT GGGGCTGGCG 120
 GCGCCGGCGG GGCCGGTGGG CTGTTACCA CCGGCGGTGT CGGCGGCGCC GGTGGGCAGG 180
 GTCACACGGG CGGGGCGGGC GCGCCGGCG GGGCCGGCGG GTTGTGTTGGT GCCGGCGGCA 240
 TGGGCGGGGC GGGCGGATTC GGGGATCACG GAACGCTCGG CACCGGCGGG GCCGGCGGG 299

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Leu Glu Pro Trp Ser Asp Gly Val Gly Leu Gly Val Asp Ser Phe Ser
 1 5 10 15
 Ala Lys Val Asn
 20

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Glu Leu Leu Phe Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly
 1 5 10 15
 Thr Asp Gly Gly Pro Gly Ala Thr Gly Gly Thr Gly Gly His Gly Gly

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20 25 30
 Val Gly Gly Asp Gly Gly Trp Leu Ala Pro Gly Gly Ala Gly Gly Ala
 35 40 45
 Gly Gly Gln Gly Gly Ala Gly Gly Ala Arg Ser Asp Gly Gly Ala Leu
 50 55 60
 Gly Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly
 65 70 75 80
 Gly Arg Gly Thr Leu Leu Leu Gly Ala Gly Gly Gln Gly Gly Leu Gly
 85 90 95
 Gly Ala Gly Gly Gln Gly Gly Thr Gly Gly Gly Arg Arg Arg Trp Arg
 100 105 110
 Ser Gly Gly Cys Gln Trp His Trp Trp
 115 120

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Gly Val Ile Gly Lys Ala Thr Ala Gln Arg Pro Val Ala Ala Gly Arg
 1 5 10 15
 Pro Arg Pro Arg Pro Gln Arg Pro Val Ser Asp Arg Val Ser Asp Gln
 20 25 30
 Arg Arg

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Leu Val Gly Gly Ile Gly Gly Thr Gly Gly Thr Gly Gly Asn Ala Gly
 1 5 10 15
 Met Leu Ala Gly Ala Ala Gly Ala Gly Gly Ala Gly Gly Phe Ser Phe
 20 25 30
 Ser Thr Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe
 35 40 45
 Thr Thr Gly Gly Val Gly Gly Ala Gly Gly Gln Gly His Thr Gly Gly
 50 55 60
 Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe Gly Ala Gly Gly Met
 65 70 75 80

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Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly
 85 90 95
 Ala Gly Gly

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TCCTGTTCGG	CGCCGGCGGG	GTGGGCGGTG	TTGGCGGTGA	CGGTGTGGCA	TTCCTGGGCA	60
CCGCCCCCGG	CGGGCCCGGT	GGTGCCGGCG	GGGCCGGTGG	GCTGTTTCAGC	GTCCGGTGGGG	120
CCGGCGGCGC	CGGCGGAATC	GGATTGGTCG	GGAACAGCGG	TGCCGGGGGG	TCCGGCGGGT	180
CCGCCCTGCT	CTGGGGCGAC	GGCGGTGCCG	GCGGCGCGGG	TGGGGTTCGGG	TCCACTACCG	240
GCGGTGCCGG	CGGGGCGGGC	GGCAACGCCA	GCCTGCTGGT	AA		282

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

CGGCACGAGC	CGTGCTACTG	GTCAACTGAT	GCCCTGATTG	TGACCTTCCC	GGCGCCGGAT	60
CAGTGCTTCT	CAGGACCGAC	GTAATATTCG	AAAACCAATC	CGGCCGCCGA	GGCGAGGATG	120
AATGCCACAC	CGGCGGCGAT	CAGCCACGGG	AGCCACAACG	CGATGCCGAC	CGCTGCCACC	180
GAGCCGGACA	ACGCGACCAT	GATCGGCCAC	CAGCTATGCG	GA CTGAAGAA	TCCAAGTTCT	240
CCTGCGCCGT	CGCTGATTTC	AGCGCCTTCG	TAGTCCTCGG	GCCGGGAATC	TAACCGGCGG	300
GCCACAAACC	GGAAGAAGGT	GGCGACGATC	AACGCCATGC	CGCCGGTGAG	CGCCAACGCA	360
ATGGTGCCAG	CCCACTCGAC	ACCACCGGTG	GCGAACATCG	AGGTCAACAC	GCCGT	415

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

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TCACCGCGTG	AACGGTTCGT	AACACTGATA	CGTATGCTTG	TCAGCGAGCA	GATCAAGTCC	60
AGTCCGACCA	ATGCCAGGAG	ATCATCGGCT	AGGCTCACGG	TTTCGCCTGG	GACGAGACGG	120
TATTGAGTTC	TGGCGTTGGA	CGGTCCGTGG	CGTGGTGGGA	AGTCTGACGC	GGCATCAGAA	180
CGGTTGTCAA	TACCAGTCTT	TGGGGGATAT	GGCCTATTTG	GTGTCGTCGG	GCCGCTCCAC	240
CGGATCCCTT	TTTCAACGTT	GCGCAAGCGC	GGTCCAGTTA	CGGCCTGTTC	ACTGCGCGCT	300
GGCGTAGCTG	CGCGGCCTCG	ATCGGTTTGA	ACGTCATCGC	AATCCCCGCA	ATGGGTGAGT	360
ACCTGACGCT	CCT					373

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

CCAAACCGGA	CAGGCCGGCA	GCGACGGTCG	GAAGTTGCAC	CACGGTGC GC	GCTCCATGTA	60
GCCAACCGGT	GACCACGGCG	TAGACAGCAG	ATCCGTGGAT	CGCGCGTTCG	GTGTCGTCCG	120
GGCCGAGTAC	CCGCGGGCCG	AACCGCAGCG	ACCAAAGCAA	CGCGATCGAT	ACGGGGATCG	180
CCACTCGTGC	CGAATTCGAG	CTCCGTCGAC	AAGCTTGCGG	CCGCACTCGA	ACCCGGGTGA	240
ATGATTGAGT	TTAAACCGCT	TAGCAATAAC	TAGCATAACC	CCTTGGGGCC	TCTAAACGGG	300
TCTTGAGGGG	TTTTTTGCTG	AAAGGAGGAA	CTATATCCGG	ATAACCTGGC	GTAGTAGCGA	360
AGAGGCCCGC	ACCGATCGCC	CTTCCCAACA	GTTGCGCAGC	CTGAATGGCG	AATGGACGCG	420
CCC						423

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

AGTGGCCAGC	CGGTCCGCCA	ATGCATCCAG	CTCCCGGTAC	GTCAGCTGAC	CATCCGCCCA	60
ACTGACCGCC	ACCGAGTCAG	GCTGTGCCGC	AGCGATTTCG	GCGAACCGGG	TATGCACCGC	120
GGGTGCCGAC	GTCGTACAT	CCGGCAGGCC	GGGTGCGGTC	GGATCGTGCT	CGCCGTCCAG	180
CAGAATGTCG	ACGTCGCGCA	GCGGCCGATC	CCACCGGCTG	ACCAAGCGCT	GTAACACAGC	240
CAGCACCCGC	CTGCCGAGGC	TTTCGGGCGC	CATCGTGCCC	AGCGCACCGT	CGAGCACCTC	300
CACTAGCAGC	GTGAGCTCAC	CGGTGCTGCG	GTGCGCGGCG	ACGGTCACCG	GAAAGTGCGA	360
CAAACCTCT	AGCGCCACCG	GACGGAACGT	CACCCCGTTT	GCGA		404

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GTCCTGGTCG	CAGGCTGTTC	TTCGAACCCG	CTGGCTAACT	TCGCACCCGG	GTATCCGCCC	60
ACCATCGAAC	CCGCCCCAACC	GGCGGTGTCA	CCGCCTACTT	CGCAAGACCC	GGCCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCACTATTCTG	ACAACGGCAC	CCGCCAATTG	180
GTGGCTCTGC	GCCCCGGGCGC	CGATTCTGGCG	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
ATGCACGTTG	CACCGCGCGT	CATTTTCTG	CCGGGCCCGG	CAGCCGCGTT	GACCAGCGAC	300
GACCACGGCA	CGGCCTTCCT	TGCCGCCCCG	GGCGGCTACT	TCGTGGCCGA	CCTGTCCTCC	360
GGTCACACCG	CACGAGTGAA	TGTCGCTGAC	GCAGCGCACA	CCGATTTCAC	CGCGATCGCC	420
C						421

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATGCATATCA	CGCTCAACGC	CATCCTGCGT	GCGATCTTCG	GGGCCGGCGG	CAGTGAACCTA	60
GACGAGCTGC	GCCGCCTCAT	TCCGCCGTGG	GTCACGCTGG	GCTCGCGCCT	GGCGGCGCTA	120
CCGAAACCCA	AACGCGACTA	TGGCCGCCTT	AGCCCCGTGGG	GCCGGCTGGC	CGAGTGGCGG	180
CGCCAGTACG	ACACTGTCAT	CGACGAGCTC	ATCGAAGCCG	AGCGGGCCGA	CCCGAACTTC	240
GCCGATCGGA	CCGACGTTTT	GGCGTTGATG	CTGCGCAGCA	CTTACGACGA	CGGTTCCATC	300
ATGTCGCGCA	AGGACATTGG	CGACGAACTG	CTCACGCTGC	TTGCCGCCGG	GCACGAAACC	360
ACGGCGGCGA	CATGGGCTGG	GCGTTCGAAC	GGCTCAACCG	GCACCCCGAC	GTGCTCGCGG	420
CTCTGG						426

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GTCCTGGTCG	CAGGCTGTTC	TTCGAACCCG	CTGGCTAACT	TCGCACCCGG	GTATCCGCCC	60
ACCATCGAAC	CCGCCCCAACC	GGCGGTGTCA	CCGCCTACTT	CGCAAGACCC	GGCCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCACTATTCTG	ACAACGGCAC	CCGCCAATTG	180
GTGGCTCTGC	GCCCCGGGCGC	CGATTCTGGCG	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
GTGCACGTTG	CACCGCGCGT	CATTTTCTG	CCGGGCCCGG	CAGCCGCGTT	GACCAGCGAC	300
GACCACGGCA	CGGCCTTCCT	TGCCGCCCCG	GGCGGCTACT	TCGTGGCCGA	CCTGTCCTCC	360
GGTCACACCG	CACGAGTGAA	TGTCGCTGAC	GCAGCGCACA	CCGATTTCAC	CGCGATCGCC	420

20250220 10084843

CGCCGCTCCG ACGGCAAGCT GGTGCTGGGC AGCGCAGATG GCGCCGTCTA CACGCTTGCC 480
AAGAACCCGC AGTTGACCGG CGTCGGCGCC GCCACCGTAG CC 522

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GCTGGGGCGC	ACCGCCGTCC	GGCGGCCCCA	GCCCCTGGGC	CCAGACCCCG	CGCAAAACCA	60
ACCCGTGGCC	CTTAGTGGCC	GGCGCCGCCG	CCGTCGTGCT	CGTCCTCGTG	TTGGGCGCCA	120
TCGGCATCTG	GATCGCCATC	CGGCCAAAGC	CGGTACAGCC	GCCTCAGCCG	GTTGCGGAGG	180
AGCGCCTTAG	CGCCCTACTG	CTGAACTCCT	CAGAAGTCAA	CGCCGTGATG	GGCTCGTCGT	240
CCATGCAGCC	GGGCAAACCG	ATCACATCGA	TGGACTCTTC	GCCGGTGACG	GTGTCCCTGC	300
CGGACTGCCA	GGGCGCGCTG	TATACCAGCC	AGGATCCGGT	GTATGCCGGC	ACCGGCTACA	360
CCGCCATCAA	CGGCTTGATT	TCATCCGAGC	CGGGCGACAA	CTACGAACAT	TGGGTGAACC	420
AAGCCGTCGT	CGCCTTTCGG	ACCGCCGACA	AAGCCCGCGC	GTTTCGTGCAG	ACTTCGCGCC	480
ACAAATGGAA	GAAGTGCACA	GGCAAGACGG	TCACCGTCAC	GAATAAGGCC	AAGACCTACC	540
GGTGGACGTT	TGCCGACGTC	AAAGGCAGCC	CGCCGACGAT	CACGGTGATA	GACACCCAAG	600
AAGGCGCTGA	GGGCTGGGAA	TGCCAACGCG	CGATGAGCGT	GGCCAACAAT	GTGGTTGTCT	660
ACGTCAACGC	ATGCGGGTAC	CAGATCACCA	ATCAAGCAGG	CCAGATCGCC	GCCAAGATCT	720
GTTGACAAAG	TCAACAAG					739

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

AGACGTCGTC	GAGGCCGCCA	TCGCCCCGCG	CGAAGCCGTT	AACCCGGCAC	TGAACGCGTT	60
GGCGTATGC						69

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

2005220 E4848001

ACTGCACCCG	GCAGGCGCGA	CCAACGGATC	GGGTCAACTA	GCACTGCCGG	TGGAGGCGCC	60
CCCGCGGTCT	GTGCCTTCCC	ACGGGGAACC	CTTGGGCAGC	GCGGCTCCAG	AAGGGTTGGA	120
GGGAGAGTTC	GACGACCGTA	TCGACGAGCG	GTTCCCGGTC	TTCAGCTCGG	CCAGTCTCGC	180
CGAAGCGCTG	CCGGGTCCGC	TGACCCCGAT	GACGCTGGAT	GTCCAGTTGA	GTGGACTGCG	240
CGCGGCCGGT	CGGGCGATGG	GTCGGGTACT	GGCGCTTGGC	GGTGTCTGTT	CCGATGAGTG	300
GGAGAGAAGA	GCCATCGCGG	TGTTCCGGTCA	CCGCCCGTAT	ATCGGAGTGT	CGGCCAATAT	360
TGTGGCCGCC	GCCCAACTGC	CGGGGTGGGA	CGCGCAGGCC	GTAACCCGGC	GGGCACTGGG	420
CGAGCAACCG	CAGGTCACTG	AGCTGCTTCC	GTTTGGTCGA	CCGCAACTTG	CGGGCGGACC	480
GCTCGGCTCG	GTCGCGAAGG	TGGTCGTGAC	GGCACGGTCG	CTG		523

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GTGTCGGTGT	CGTCGGGGTA	GGAGCGACTT	CCCCGGCCGG	CGCCGGCGCC	GGAGCGGGCT	60
CTGCAGGAAC	CGGTGCCGGC	GCCGGCGGCG	GGGCGACCAA	AGGCCGGATC	GATTCGGCCA	120
GCGCCTTGGC	CGCGCCCTTG	TCCACCGGGT	TGTTGGCGGT	CCCAGCCAT	ACCACAAACC	180
AACGCTGAAG	GGGCCC GGCG	TCCGGTGCGT	TCGCCGCGGG	CGAC		224

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TGAACTGACT	GCCCCGCTCG	ATCGGCGGCG	GCGGCGTGTC	ATAGCTGCGC	CGCCAGGCCA	60
TGAACTGCTC	TTCGCCATAG	CGGGCCTTGG	TCTCGGCCCTT	GTCCAAACCC	TGCAGCGCGC	120
CGTAGTGGCG	TTCGTTGAGC	CGCCAGCTAC	GCCGCACGGG	AATCCAGAGC	CGATCGGCGC	180
TGTCCAACGC	CAGATGCGCG	GTGGTGATCG	CGCGCCGCAG	CAACGAGGTG	TAGAGCACGT	240
CGGGCAATAG	GTCGTGTTCC	GCGATCAGCT	CGCCGCTTCG	AACCGCCTCT	GCCTGGCCCT	300
TGTCCGTCAG	GCCGACATCG	ACCCAGCCGG	TGAACAGGTT	GAGGGCATTG	CAGTCGCTCT	360
CGCCGTGGCG	CAGCAACACC	AGGCTGCCAG	TGTTTGCCAT	ACCGGCAAGT	CTCTCACGCA	420
CTCCCGCACT	CCTCATCGTG	GACCAAAATG	CCCGAATTCT	CCTCGGTCCG	CTGCGCAGCG	480
CGTTCATACC	GCCGAGGTGG	TCGGCACCGT	AACGGCCGGT	T		521

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTCCAGGCTC	ATTCGCTCGA	ACAAAGCCAC	CCGGCCGTAC	AGCGGACGCC	CCCATTCTGTT	60
GTCGTGATAG	TCGCGGTACA	GCTGGGCATC	GGGCCCTGGA	CGAACCTCCG	CCCAGGGGCA	120
GCGAACCAGC	CCGTCGCCGC	TCACGCGGGG	TCAGAACGGT	AGTGCACGAC	AGTCTCGCCG	180
CGCGAAGGGT	TTGACGCGTC	AGACTCGGCC	TCGGCGTCTT	CCGACGAGGC	GTGGATCGCC	240
CCGAGCTGAG	AGCGTAGCGC	CTCGAGCTCA	CGGCCGAGCC	GTTCCAGCAC	CCAGTCCACC	300
TCGCTGGTCT	TGTTCCCGCG	CAGCACCTGC	GTGAACTTGA	CCGCGTCGAC	ATCGGCGCGG	360
GTGACCCCGA	ACGCCGGCAG	CGTCGTCGCC	GTCGTCGCCC	GCGGCAGGGG	CGGCAACTGC	420
TCGCCA						426

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GCGGACACGG	CGGACAAAGC	GCAATCGGCC	TCGGCGGCGG	CGCCGGCGGC	GACGGGGGGCC	60
AGGGCGGCGC	CGGCCGCGGA	CTGTGGGGTA	CTGGCGGCGC	CGGCGGACAC	GGCGGGGCAA	120
GGCGGTGGTA	CCGGGGGGCC	ACCGCTGCCC	GGTCAGGCAG	GCATGGGCGC	CGCGGGTGGC	180
GCCGGTGGGC	TGATCGGCAA	CGGCGGGGCC	GGCGGCGAC			219

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AAGATCATCG	GCGCCGCTCC	TTAGCATCGC	TGCGCTCTGC	ATCGTCGCCG	GCGCGGATCA	60
CGGAGGTCCG	GCCTTGTACC	CCACTCCTCG	AACGGTCAGC	ACCACAGTCG	GGTTCCTCGG	120
ATCCTTTTCG	ACCTTGGCCC	GCAGACGCTG	GACATGCACG	TTCACCAGCC	TGGTATCGGC	180
TGGGTGCCGG	TAACCCATA	CCTGTTCGAG	CAGCACATCA	CGAGTAAACA	CCTGGCGCGG	240
CTTGCGCGCC	AATGCGACCA	ACAGGTCGAA	TTCCAGCGGT	GTCAACGAGA	TCTGCTCACC	300
GTTGCGAGTG	ACCTTGTGCG	CCGGTACGTC	GATTTCTACG	TCGGCGATGG	ACAGCATCTC	360
GGCGGGTTTC	TCGTCGTTGC	GGCGCAGCCG	CGCCCGCACC	CGCGCAACCA	GCTCCTTGGG	420
CTTGAACGGC	TTCATGATGT	AGTCGTCGGC	GCCCGACTCC	AGACCCAGCA	CCACATCCAC	480
GGTGTCGGTC	TTTGCGGTGA	GCATCACGAT	CGGAACACCG	GAATCGGCGC	GCAACACCCG	540
GCACACGTCG	ATGCCGTTCA	TACCGGGGCA	A			571

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(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Leu Phe Gly Ala Gly Gly Val Gly Gly Val Gly Gly Asp Gly Val Ala
 1             5             10             15
Phe Leu Gly Thr Ala Pro Gly Gly Pro Gly Gly Ala Gly Gly Ala Gly
      20             25             30
Gly Leu Phe Ser Val Gly Gly Ala Gly Gly Ala Gly Gly Ile Gly Leu
      35             40             45
Val Gly Asn Ser Gly Ala Gly Gly Ser Gly Gly Ser Ala Leu Leu Trp
      50             55             60
Gly Asp Gly Gly Ala Gly Gly Ala Gly Gly Val Gly Ser Thr Thr Gly
65             70             75             80
Gly Ala Gly Gly Ala Gly Gly Asn Ala Ser Leu Leu Val
      85             90

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Pro Pro Val Ser Ala Asn Ala Met Val Pro Ala His Ser Thr Pro
 1             5             10             15
Pro Val Ala Asn Ile Glu Val Asn Thr Pro
      20             25

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

10034843.022502

Lys Pro Asp Arg Pro Ala Ala Thr Val Gly Ser Cys Thr Thr Val Arg
 1 5 10 15
 Ala Pro Cys Ser Gln Pro Val Thr Thr Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Trp Pro Ala Gly Arg Pro Met His Pro Ala Pro Gly Thr Ser Ala Asp
 1 5 10 15
 His Pro Pro Asn
 20

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1 5 10 15
 Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
 20 25 30
 Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
 35 40 45
 Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
 50 55 60
 Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
 65 70 75 80
 Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
 85 90 95
 Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
 100 105 110
 Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala
 130 135 140

(2) INFORMATION FOR SEQ ID NO:282:

10034343-022502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly
 1           5           10           15
Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr
          20           25           30
Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly
          35           40           45
Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Gln Tyr Asp
          50           55           60
Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn Phe
          65           70           75           80
Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp
          85           90           95
Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr
          100          105          110
Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg
          115          120          125
Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1           5           10           15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
          20           25           30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
          35           40           45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
          50           55           60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
          65           70           75           80
Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
          85           90           95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
          100          105          110

```

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Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp
 130 135 140
 Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala
 145 150 155 160
 Lys Asn Pro

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro
 1 5 10 15
 Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Ala Val Val
 20 25 30
 Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro
 35 40 45
 Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala
 50 55 60
 Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser
 65 70 75 80
 Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr
 85 90 95
 Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro
 100 105 110
 Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser
 115 120 125
 Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala
 130 135 140
 Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp
 145 150 155 160
 Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala
 165 170 175
 Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr
 180 185 190
 Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln
 195 200 205
 Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys
 210 215 220
 Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

10084843-022502

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
 1           5           10           15
Leu Asn Ala Leu Ala Tyr
           20

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
 1           5           10           15
Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
           20           25           30
Ser Ala Ala Pro Glu Gly Leu Glu Gly Glu Phe Asp Asp Arg Ile Asp
           35           40           45
Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
           50           55           60
Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
           65           70           75           80
Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
           85           90           95
Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
           100          105          110
Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Ala Gln Leu Pro Gly
           115          120          125
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln
           130          135          140
Val Thr Glu Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro
           145          150          155          160
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu
           165          170

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Val	Gly	Val	Val	Gly	Val	Gly	Ala	Thr	Ser	Pro	Ala	Gly	Ala	Gly	Ala
1				5					10				15		
Gly	Ala	Gly	Ser	Ala	Gly	Thr	Gly	Ala	Gly	Ala	Gly	Gly	Gly	Ala	Thr
			20					25					30		
Lys	Gly	Arg	Ile	Asp	Ser	Ala	Ser	Ala	Leu	Ala	Ala	Pro	Leu	Ser	Thr
		35					40					45			
Gly	Leu	Leu	Ala	Val	Pro	Ser	His	Thr	Thr	Asn	Gln	Arg			
		50					55				60				

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met	Ala	Asn	Thr	Gly	Ser	Leu	Val	Leu	Leu	Arg	His	Gly	Glu	Ser	Asp
1				5					10				15		
Trp	Asn	Ala	Leu	Asn	Leu	Phe	Thr	Gly	Trp	Val	Asp	Val	Gly	Leu	Thr
			20					25					30		
Asp	Lys	Gly	Gln	Ala	Glu	Ala	Val	Arg	Ser	Gly	Glu	Leu	Ile	Ala	Glu
		35					40					45			
His	Asp	Leu	Leu	Pro	Asp	Val	Leu	Tyr	Thr	Ser	Leu	Leu	Arg	Arg	Ala
		50				55					60				
Ile	Thr	Thr	Ala	His	Leu	Ala	Leu	Asp	Ser	Ala	Asp	Arg	Leu	Trp	Ile
65				70					75				80		
Pro	Val	Arg	Arg	Ser	Trp	Arg	Leu	Asn	Glu	Arg	His	Tyr	Gly	Ala	Leu
			85					90					95		
Gln	Gly	Leu	Asp	Lys	Ala	Glu	Thr	Lys	Ala	Arg	Tyr	Gly	Glu	Glu	Gln
			100					105					110		
Phe	Met	Ala	Trp	Arg	Arg	Ser	Tyr	Asp	Thr	Pro	Pro	Pro	Pro	Ile	Glu
		115					120					125			
Arg	Gly	Ser	Gln	Phe											

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

205220" CH84800T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Pro Gly Ser Phe Ala Arg Thr Lys Pro Pro Gly Arg Thr Ala Asp Ala
 1           5           10           15
Pro Ile Arg Cys Arg Asp Ser Arg Gly Thr Ala Gly His Arg Ala Leu
          20           25           30
Asp Glu Pro Pro Pro Arg Gly Ser Glu Pro Ala Arg Arg Arg Ser Arg
          35           40           45
Gly Val Arg Thr Val Val His Asp Ser Leu Ala Ala Arg Arg Val
 50           55           60

```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly Gly
 1           5           10           15
Asp Gly Gly Gln Gly Gly Ala Gly Arg Gly Leu Trp Gly Thr Gly Gly
          20           25           30
Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala
          35           40           45
Ala Arg Ser Gly Arg His Gly Arg Arg Gly Trp Arg Arg Trp Ala Asp
 50           55           60
Arg Gln Arg Arg Gly Arg Arg Arg
 65           70

```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```

Asp His Arg Arg Arg Ser Leu Ala Ser Leu Arg Ser Ala Ser Ser Pro
 1           5           10           15
Ala Arg Ile Thr Glu Val Arg Pro Cys Thr Pro Leu Leu Glu Arg Ser
          20           25           30
Ala Pro Gln Ser Gly Ser Arg Asp Pro Phe Arg Pro Trp Pro Ala Asp
          35           40           45
Ala Gly His Ala Arg Ser Pro Ala Trp Tyr Arg Leu Gly Ala Gly Asn
 50           55           60

```

205220" CH2H300T

Pro Ile Pro Val Arg Ala Ala His His Glu
65 70

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

CCGCACGTAA CACCGTGAAT TGAAGGGAGC CGCTGGTCAT GGGCCGATTC TATCCGTGGG	60
CGAACGGTTA TTGACGGCCC GGAGGCCACT CCGCTGCCAC CAAGTGGTGA CTCAGCGCGT	120
TTTCACGGCA ACGAACGGCG GACACACCAC TTGACATTCG ACAGCACGGC CGCG	174

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

TCGCAAACGG GGTGACGTTT CGTCCGGTGG CGCTAGAGAG TTTGTCGCAC TTTCCGGTGA	60
CCGTGCGCCG GCACCGCAGC ACCGGTGAGC TCACGCTGCT AGTGGAGGTG CTCGACGGTG	120
CGCTGGGCAC GATGGCGCCC GAAAGCCTCG GCAGGCGGGT GCTGGCTGTG TTACAGCGCT	180
TGGTCAGCCG GTGGGATCGG CCGCTGCGCG ACGTCGACAT TCTGCTGGAC GGCGAGCACG	240
ATCCGACCGC ACCCGGCCTG CCGGATGTGA CGACGTCGGC ACCCGCGGTG CATAACCGGT	300
TCGCCGAAAT CGCTGCGGCA CAGCCTGACT CGGTGGCGGT CAGTTGGGCG GATGGTCAGC	360
TGACGTACCG GGAGCTGGAT GCATTGGCCG ACCGGCTGGC CACT	404

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Ala Asn Gly Val Thr Phe Arg Pro Val Ala Leu Glu Ser Leu Ser His	
1 5 10 15	
Phe Pro Val Thr Val Ala Ala His Arg Ser Thr Gly Glu Leu Thr Leu	
20 25 30	

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Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser
 35 40 45
 Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp
 50 55 60
 Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp
 65 70 75 80
 Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val
 85 90 95
 His Thr Arg Phe Ala Glu Ile Ala Ala Gln Pro Asp Ser Val Ala
 100 105 110
 Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu
 115 120 125
 Ala Asp Arg Leu Ala Thr
 130

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GCTTCGACGG	CTACGAGTAC	CTGTTCTGGG	TGGGTTGTGC	GGGCGCCTAC	GACGACAAGG	60
CCAAGAAGAC	CACCAAGGCC	GTCGCCGAGC	TGTTCCGCGT	CGCCGGGGTG	AAATACTTGG	120
TGCTGGGCGC	TGGGGAAACC	TGCAACGGCG	ACTCGGCGCG	CCGCTCCGGC	AACGAGTTCC	180
TCTTCCAGCA	GCTGGCACAA	CAGGCCGTCG	AGACCCTGGA	CGGTTTGTTC	GAGGGTGTGG	240
AGACCGTCGA	CCGCAAGATC	GTTGTCACTT	GCCCGCACTG	CTTCAACACC	ATCGGCAAGG	300
AATATCGGCA	GCTGGGCGCC	AACTACACCG	TGCTGCACCA	CACCCAGCTG	CTCAATCGGT	360
TGGTGC CGCA	CAAGAGGCTG	GTCCCTGTCA	CTCCGGTTTC	TCAGGACATC	ACCTACCACG	420
ACCCGTGCTA	CCTGGGTCGG	CACAACAAGG	TCTACGAGGC	ACCACGGGAG	CTGATCGGTG	480
CCGCGGGGGC	CACCTGAGCC	GAGATGCCGC	GCCATGCCGA	CCGCAG		526

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CTCGCCGCCG	TGATCTGGCC	GGCGAACTTC	GTCAGTGCAT	CCAGACCCCA	ACGATCATCG	60
ATCAGGCCGA	TGCCCATGAT	CACCGCACCG	GCCACCAGCA	CCGCGGGCAT	GCCGGTGGAA	120
TAGACGAACC	CCCGGGTGAG	TGCCGGAAGC	TGGGAGGCAA	GAAAGACGGC	GCCGACAATG	180
CCCAGGAACA	TCGCCAACCC	ACCCATCCGA	GGGGTAGGCG	TGACGTGCAC	ATCTCGCTCC	240
CGCGGGTAGG	CGACGGCTCC	CAGGCGACTG	GCCAGCATCC	GCACCGGACC	GGTCGCAAAA	300
TAGGTGATGA	TCGCCGCGGT	CAGCCCGACC	AGCGCAAGCT	CACGCAGCGG	GACACCGGCG	360

CCGCGATAGG ACAGGGCGAG CAAGCCACCG GCAACGCCGG CCACATCGCT GGACACCTCG 420
 AGACCGTACT GCACCAACCT GAAGAGCTGA AACTCGCCG AACGTGCAAC AGCTGCGAAC 480
 AATTGGG 487

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

ACGAAGCGCG AGAATATGAG CCGGGGCAAC CCGGCATGTA CGAGCTTGAG TTCCCGGCGC 60
 CTCAGCTGTC GTCGTCCGAC GGCCGTGGTC CGGTGTTGGT GCACGCTTTG GAAGGTTTCT 120
 CCGACGCCGG CCATGCGATC CGGCTGGCCG CCGCCCACCT CAAGGCGGCC CTGGACACAG 180
 AGCTGGTTCG GTCCTTCGCG ATCGATGAAC TACTGGACTA CCGCTCGCGG CGGCCATTAA 240
 TGACTTTCAA GACCGATCAT TTCACCCACT CCGATGATCC TGAGCTAAGC CTGTATGCGC 300
 TGCGCGACAG CATCGGCACC CCATTTCTGC TGCTGGCGGG TTTGGAGCCG GACCTGAAGT 360
 GGGAGCGGTT CATCACC GCC GTCCGATTGC TGGCCGAGCG CCTGGGTGTA CGGCAGAACC 420
 ATCGGCCTGG GCACCGTCCC GATGGCCGTT CCGCACACAC GACCGATCAC GATGACCGCT 480
 CATTCCAACA ACCGGGAGCT ATCTCCGATT TTCAACCGTT CGATCTCC 528

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

CCAAGCCCGT CAAGGAGCCG GTGCCGGCCT TGCTCCGGT GCCGCCGACG CCGGCGTTGC 60
 CGCCGTTGCC GCCGTTGCCG CCGGTACCGG GGTTCCTAC GGTGCCGCCG CCCGGCAGCA 120
 TGGCCCCGCT GTTTAGGCCG TTTTCGCCCG CCCC GCCGTC ACCGGCTTTG CCGCCATCGC 180
 CGCCGTTGCC GCCGCTGGTG GGGGTGGCGG CCTGGTTGAC GTATTGTTCC ACCGGCCCCG 240
 CCCTTGACCC TTTGGCGGTG TCGATCGCGG CGTCGATGGA TCCGCCGACC ACGACGTGCG 300
 AAGCCTCGCC TGCCGCCGCA GCCGCCCAAC TGTGTCGCGG CTCCTGCGAT TTGGCCCCCG 360
 CCGACGAGAT GATGGGCACC ACCGGAGCCT GCGGCCGTCT GGGGGAGGCC AGCGCGGGTT 420
 CGCGGTCACG CCATACGCGA CCGTGCGCCG CCGCTTCGGA GATTTCAGG CTGCGTTGCA 480
 CCAGATCGAG CAGCGGTGTG CCCAGGGACT GGGTTAGCCC GTTGGCGCCG CCGTTGTAGC 540
 GCGGAGCGCA ATATCGGTGC CCACTCGACC CAACCGCGAC TCCATAAGCG ACACCATTGC 600
 CGGTTGATGC 610

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Phe	Asp	Gly	Tyr	Glu	Tyr	Leu	Phe	Trp	Val	Gly	Cys	Ala	Gly	Ala	Tyr	1	5	10	15
Asp	Asp	Lys	Ala	Lys	Lys	Thr	Thr	Lys	Ala	Val	Ala	Glu	Leu	Phe	Ala	20	25	30	
Val	Ala	Gly	Val	Lys	Tyr	Leu	Val	Leu	Gly	Ala	Gly	Glu	Thr	Cys	Asn	35	40	45	
Gly	Asp	Ser	Ala	Arg	Arg	Ser	Gly	Asn	Glu	Phe	Leu	Phe	Gln	Gln	Leu	50	55	60	
Ala	Gln	Gln	Ala	Val	Glu	Thr	Leu	Asp	Gly	Leu	Phe	Glu	Gly	Val	Glu	65	70	75	80
Thr	Val	Asp	Arg	Lys	Ile	Val	Val	Thr	Cys	Pro	His	Cys	Phe	Asn	Thr	85	90	95	
Ile	Gly	Lys	Glu	Tyr	Arg	Gln	Leu	Gly	Ala	Asn	Tyr	Thr	Val	Leu	His	100	105	110	
His	Thr	Gln	Leu	Leu	Asn	Arg	Leu	Val	Arg	Asp	Lys	Arg	Leu	Val	Pro	115	120	125	
Val	Thr	Pro	Val	Ser	Gln	Asp	Ile	Thr	Tyr	His	Asp	Pro	Cys	Tyr	Leu	130	135	140	
Gly	Arg	His	Asn	Lys	Val	Tyr	Glu	Ala	Pro	Arg	Glu	Leu	Ile	Gly	Ala	145	150	155	160
Ala	Gly	Ala	Thr																

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Arg	Arg	Arg	Asp	Leu	Ala	Gly	Glu	Leu	Arg	Gln	Cys	Ile	Gln	Thr	Pro	1	5	10	15
Thr	Ile	Ile	Asp	Gln	Ala	Asp	Ala	His	Asp	His	Arg	Thr	Gly	His	Gln	20	25	30	
His	Arg	Gly	His	Ala	Gly	Gly	Ile	Asp	Glu	Pro	Pro	Gly	Glu	Cys	Arg	35	40	45	
Lys	Leu	Gly	Gly	Lys	Lys	Asp	Gly	Ala	Asp	Asn	Ala	Gln	Glu	His	Arg	50	55	60	
Gln	Pro	Thr	His	Pro	Arg	Gly	Arg	Arg	Asp	Val	His	Ile	Ser	Leu	Pro	65	70	75	80
Arg	Val	Gly	Asp	Gly	Ser	Gln	Ala	Thr	Gly	Gln	His	Pro	His	Arg	Thr	85	90	95	
Gly	Arg	Lys	Ile	Gly	Asp	Asp	Arg	Arg	Gly	Gln	Pro	Asp	Gln	Arg	Lys				

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	100		105		110										
Leu	Thr	Gln	Arg	Asp	Thr	Gly	Ala	Ala	Ile	Gly	Gln	Gly	Glu	Gln	Ala
	115					120					125				
Thr	Gly	Asn	Ala	Gly	His	Ile	Ala	Gly	His	Leu	Glu	Thr	Val	Leu	His
	130					135					140				
Gln	Pro	Glu	Glu	Leu	Asn	Thr	Arg	Arg	Thr	Cys	Asn	Ser	Cys	Glu	Gln
145					150					155				160	
Leu															

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Glu	Ala	Arg	Glu	Tyr	Glu	Pro	Gly	Gln	Pro	Gly	Met	Tyr	Glu	Leu	Glu
1			5					10					15		
Phe	Pro	Ala	Pro	Gln	Leu	Ser	Ser	Ser	Asp	Gly	Arg	Gly	Pro	Val	Leu
	20						25					30			
Val	His	Ala	Leu	Glu	Gly	Phe	Ser	Asp	Ala	Gly	His	Ala	Ile	Arg	Leu
	35					40					45				
Ala	Ala	Ala	His	Leu	Lys	Ala	Ala	Leu	Asp	Thr	Glu	Leu	Val	Ala	Ser
	50				55				60						
Phe	Ala	Ile	Asp	Glu	Leu	Leu	Asp	Tyr	Arg	Ser	Arg	Arg	Pro	Leu	Met
65				70				75					80		
Thr	Phe	Lys	Thr	Asp	His	Phe	Thr	His	Ser	Asp	Asp	Pro	Glu	Leu	Ser
		85				90						95			
Leu	Tyr	Ala	Leu	Arg	Asp	Ser	Ile	Gly	Thr	Pro	Phe	Leu	Leu	Leu	Ala
	100					105					110				
Gly	Leu	Glu	Pro	Asp	Leu	Lys	Trp	Glu	Arg	Phe	Ile	Thr	Ala	Val	Arg
	115				120						125				
Leu	Leu	Ala	Glu	Arg	Leu	Gly	Val	Arg	Gln	Asn	His	Arg	Pro	Gly	His
	130				135					140					
Arg	Pro	Asp	Gly	Arg	Ser	Ala	His	Thr	Thr	Asp	His	Asp	Asp	Arg	Ser
145				150				155						160	
Phe	Gln	Gln	Pro	Gly	Ala	Ile	Ser	Asp	Phe	Gln	Pro	Phe	Asp	Leu	
			165					170					175		

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10084843 "022502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Lys Pro Val Lys Glu Pro Val Pro Ala Leu Pro Pro Val Pro Pro Thr
 1 5 10 15
 Pro Ala Leu Pro Pro Leu Pro Pro Leu Pro Pro Val Pro Gly Phe Pro
 20 25 30
 Thr Val Pro Pro Gly Ser Met Ala Pro Leu Phe Arg Pro Phe Ser
 35 40 45
 Pro Ala Pro Pro Ser Pro Ala Leu Pro Pro Ser Pro Pro Leu Pro Pro
 50 55 60
 Leu Val Gly Val Ala Ala Trp Leu Thr Tyr Cys Ser Thr Gly Pro Ala
 65 70 75 80
 Leu Asp Pro Leu Ala Val Ser Ile Ala Ala Ser Met Asp Pro Pro Thr
 85 90 95
 Thr Thr Cys Glu Ala Ser Pro Ala Ala Ala Ala Gln Leu Cys Arg
 100 105 110
 Gly Ser Cys Asp Leu Ala Pro Ala Asp Glu Met Met Gly Thr Thr Gly
 115 120 125
 Ala Cys Gly Arg Leu Gly Glu Ala Ser Ala Gly Ser Arg Ser Arg His
 130 135 140
 Thr Arg Arg Cys Ala Ala Ala Ser Glu Ile Cys Arg Leu Arg Cys Thr
 145 150 155 160
 Arg Ser Ser Ser Gly Val Pro Arg Asp Trp Val Ser Pro Leu Ala Pro
 165 170 175
 Pro Leu

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

AATTCGGCAC	GARCAGCACC	AACACCGGCT	TCTTCAACTC	CGGCGACGTC	AATACCGGTA	60
TCGGCAACAC	CGGCAGCTTC	AACACCGGCA	GCTTCAATCC	GGGCGATTCC	AACACCGGGG	120
ATTTCAACCC	ANGCAGCTAC	CACACGGGGA	CTCGGAAACA	CCGGCGATTT	TACACCGGCS	180
CCTTCATCTC	CGGCAGCTAC	AGCAACGGGT	CTTGTGGAGT	GGAAATTATC	AGGGCTCAT	240
GGNTGCACCC	GGSCCTRCGA	ATCCCTCGKG	CCAATTCAAC	TCCTCNACAA	GCTTGCGGCC	300
GCACTCSAGC	CCGGGTGAAT	GATTGAGTTT	AACCGCTNAN	CAATAACTAG	CATAACCCCT	360
TKGGGCCTCT	AAACGGGTCT	TGAAGGGTTT	TTTGCTGAAA	GGANGAACTA	TATCCGGATA	420
ACTGGCGTAN	TACGAAAAGC	CGCACCAGATC	GCCTTCCCAA	CAGTTGCGCA	CCKGAATGGC	480
AATGGACCNC	CCTKTTACCG	GSCATTAACN	CGGGGGTGTTN	GGKGTACCC	CCACGTNACC	540
GCTACCTTGC	CANNSSCCTN	RSGCCGTCTT	TCSTTTCTTC	CTTCCTTCTC	CCMCTTCGCC	600
GGTTCCCNTC	AGCTCTAAAT	CGGGGNNCCC	TTTMGGGTTC	CAATTATTGC	TTACNGSCCC	660
CCACCCCAAA	AAYTNATNG	GGTTAATGTC	CCTTMTTGGG	CNTCCCCCTA	WTNANNGTTT	720
TCCCCCTTNA	CTTTGRSTCC	CTTCYTTATW	NTGAMNCTNT	TTCCACYGGA	AAAMNCTCCA	780
CCNTTYSSGS	TTTCCTTTGA	WTTATMRGGR	AATTSCAATY	CCGCYTTKGG	TTMAANTTAA	840
CYTATTTTNA	ATTTTCCCGM	TTTMMNATR	TTNSNCKCGM	KNCTCCNRKA	SSGNTTTCCT	900
CCCCCYTTSS	GKTYCCCCRN	G				921

10084843 "022502"

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

AATTCGGCAC	GAGATANGGG	CGCACCAGGG	TCCGCAGCCG	GCGGGACCGT	CGCCAGCACC	60
ACCGGGGTCA	ACAGCACCAC	GGTGGCGTCC	ANGCAGAGCG	CCGCGGTGAT	GGCGGCCGAG	120
ACGGCRAACA	CCTGCCGTAG	CAGTCGGTGC	GACTCCGCGC	TCGCTCGANC	CATGGCCGCG	180
CCGGCTGCCT	CGAACANGCC	TTCGTCGTCC	ACAGCTTAGC	CAGCANCCAA	ACCGCACCCA	240
GAAACCCACA	CGCCCGCCGC	CCCGGANACC	TGCGCCATCG	KCTGCTGGGG	CGANATCCCC	300
CGATCGCTNA	CANGATGACC	GCTGCCGGAA	CGCCGCCGCT	GCCTCCGGGC	AGCCGCGTGG	360
GCSGGGCAAC	CGCGAACCCA	NGAACACGGC	AAGCAGTATC	ANCGCAACAG	CAATTGTCAA	420
GGGCTAAACG	CTTCACATCC	AGGGATCTCG	CGGCGCCACA	CCGTCGGMTC	TGCAGSGCGA	480
CCCCNTCCTN	GGGCGGNCAC	TCNTCAAAGA	TGCNGATCNA	CAGKCTAGGT	CTTCGGCCGA	540
TATGSAAGGN	CCCAACGGNT	TTAAAGCGGC	SAAAAAATC	TCCCANTGGA	TAAAATCAGC	600
CGGGGANCCC	CCCGTGSCMM	NGTCYCGGKC	ATTNTTCAAC	MGGTTTNACG	GCGGKTGCNG	660
GCCAACTKGC	CAAAMTTAAG	KTNGGGGNTY	CGGGGCGGTA	ACCGGCNNTK	NGCCCCCTAA	720
AAAACCGGNC	YTTTCTKGAT	TAMMACCGGN	CCCCCAWTGG	CGGKTGKTCC	CANGNTYAAC	780
AMCCYCCCCS	MNGGGKTGGS	SAACCCTTCC	CGNGGGGTTC	NTKGTTSCYT	AWMCCCCCGG	840
AAACCSGKYG	GGKTGGCRTN	WASSAMNCCC	CMNGYYTCTT	TAAAGGCCAN	KNRAAWGKYT	900
CCTTGGAAW	CCTNCAATYC	GAAAAYYCTC	CTYMMGSSCN	CTTKCWRTYN	NRNGGGAACS	960
AMWTNYCCNC	GWTTCAWTCG	GGTCCGASMN	AAACKCTTTY	TTTTYCGSSC	STCCMGSNC	1020
SGGTKNANAN	AAASATTTMC	YYCNNNANKK	YYYCSSGCTT	CYKMGRNRNR	GMGAACCCGR	1080
GS						1082

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

AATTGGCACG	AGTGATCGCG	CTGAAGCCGG	TAGCGCGGGT	GGCTCGGGTG	GTTTGCGAAC	60
RAAATCCGCT	CGANGTGGTC	TCGGTAGGCG	GTGTCCANAA	CGGTGGCGCG	GTGCCGGCGG	120
ATCTGATCGG	CGCGGCCGTA	GTGCACGTCT	GCGGGCGTGT	GCAGTCCGAT	GCCGGAATGC	180
TTGTGTTCGT	GGTTGTACCA	GCCGAAGAAC	CGGTGCGAGT	GCACCCGGGC	CGCCTCGATC	240
GACTCGAACC	GTTTCGGGAA	ATCGGGCCGG	TACTTGAAGG	TCTYGAAGT	GGCCTCAGAC	300
AACGGGTTGT	CTTGCTGGTG	TGCGGGCGTG	AGTGCGACTT	GGTGACACCG	AAGTCGGCCA	360
NCANCAATGC	CACCGGTTTG	GAATCATCC	ACAACCCCCG	TCCGCGTCMA	GGTCACTTGT	420
NCGGCGCTAA	TTTNYTGGGC	GGCAAGGGTT	TGCCGAYCAN	KCCGCTCGGC	CAAACTTCG	480
ANTCNCSCCA	AGGCCNCCAT	CCNCCCAAAC	AMGTTACGGG	ANAAAANATY	CAAAGAYCAC	540
CYTCCGGKTN	TTATANCTYC	CCYTTTGSTY	GGGCCCCCN	CYYTGKKNAT	ACCCCTNCCA	600

AWTCCCAACN	CCCKCCAANA	RCYKGGGGCC	CCCNCCAACC	CGGGKGAACA	WTAATTTAAA	660
CCCYAACMAW	ACTWMMNACC	CNNGGSSCCY	AAMCGTYYNR	AGGTTTTSCT	NAAAGAAASA	720
ANTCGGAAMC	CGGNTSTACC	AAAAASCCCK	CCNWTCCCTC	CRASATTGSC	NCCSAAWKSA	780
AKGCCCCCN	TCSGCNWNNC	CSGCGGKKKT	KKGTTNCCCT	WMRCWMWYTS	GGCCNASCCN	840
CKYYSSMYCC	CCCCTCCCCM	CTCCGNKTCC	CCAMCCYANC	MGGCCCCCYTM	GKKCCCWKNT	900
YKGCCCCCCC	AMMNNNGGGG	WGACCCTNGG	CCCCMKRRGM	TCCCNANTGA	MCCTCWGNRA	960
MKCYCCNRAR	ANMCCSCNCC	NGCNCRCNN				990

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

AATTCGGGTG	GCAACGCGGG	CCTGTTCGGC	AACGGCGGCG	CCGGTGGTGC	CGGTGGGGCT	60
GGTGGTGGCG	CCGGCGGCGC	GGGCGGTAAC	GCGGGGTGGT	TTGGTCATGG	GGGCGCTGGC	120
GGCGTGGGTG	GTGTANGTGC	GGCCGGGGCC	AACGGTGCTA	CGCCCGGTCA	GGATGGGGCG	180
GCTGGTGTTC	CCGGGTCGGA	CRACRCTCGT	GCCGCTCGTG	CCG		223

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AATTCGGCAC	GANGCGGCAA	CGGTGGCAGC	GGCGGCACGT	CNGTTGCCAC	CGGGGGGGCC	60
GGGAACGGCG	GTGCCGGCGG	CGCCGGCGGC	GGGGCCGGGC	TGATCGGCAA	CGGCSGCAAC	120
GGCGGCAGTG	GCGGAATGGG	CGATGCCCCG	GGCGGCACCG	GCGTCNGCGG	CATCRGTGGG	180
CTGTTGTTGG	GTTTGGACRG	CGCCAACGCC	CCGGCCAGCA	CCAACCCGCT	GCACACCGCG	240
CAGCACAGGC	GTTGGCCGCA	GTCAACGCGC	CCATCCAGGC	CGTGACCGGG	CGCCCCTGAT	300
CGGCAACGCG	CCAACGGCGC	CCCGGGCAAC	GGGGCCCCCG	GCRGGCACGG	CGGGTGGTTG	360
TTCGGCGGCG	GAAGGAACGG	CGGGTCCGGC	GTCANCRGCG	GGGCGGGCGG	AAATGCCG	418

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

10084843.022502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTCGGCAC	GAGGGGCACG	ATCGCATACA	GCGCTCGCGG	CAGACCCGCC	CGATACAGCA	60
GCTCGGCACA	CGCGAGCGCA	CAATACGGCG	TCTGGCTGTC	CGGCTTGARC	ACCACCGCGT	120
TACCGGCCAC	CAGCGCGGGC	ACCGAGTCCG	ACACCGTAAG	CGTCATGGGG	TAGTTCCACG	180
GCGAGATCAC	CCCCACCACG	CCCTTCGGTT	GATAGCACAC	CGTGGTCTTG	CCTATCCCGG	240
GCAGCAGCGG	CTGTGCCTTA	CGGGGCTTCA	GCAGGTCCAC	ACAGACTCGT	GCSTTATAAT	300
TNCGCSTTCC	GCGATCAGAT	CGACAATTTC	CTCTTGCGCC	GCCCATCGGG	CCTTGCCCGC	360
CTCGGCTTGC	AGGAAGTCCA	TGAAGAATC	GCGGTTCTCG	ATNAACAGGT	CGCGATAGCG	420
GCSGATGACT	GCAGCTCGCT	CGATNACGGG	ACCTTCGCCA	GTCGGTCTGC	GCCGCGCGAN	480
CTTCCGCGAA	TGCCGCTTCG	ACTTCCGCGG	NCGTGCCAAC	GGAATCNTAT	CACGGGTTGC	540
CGGTAAAAAC	TCCTCAATST	NCYGGTCGAA	ATTCGGCAAC	TTCTTATCCC	GGCAGGTRCC	600
AACSANNCAA	ACCTCGGCAA	GGTTAGGMIT	TCCCCNCTT	YCAAAAATNC	GGKTTTTGGN	660
CMAATTTTCG	CKCNATGKTG	MCAAGGMTCT	CKAANAACCS	GGGTCYTCTN	NTCNGKGGAK	720
CCAAAMGGKT	TTGGGGMAGC	GKNMNCCAAN	CCTWACCCTG	KTKAANGGNW	TTCCCCCGG	780
GGGAKKNGA	ATYCYCCSNA	NCCCRGGGGG	GNMCARATTC	TYCCGGMCTC	CTCKGGAWTC	840
WGMGSTTTCC	CAAAAAACSC	CCCAAATTMM	TTTTTCCRCN	TRTTGANACW	CTTTTKARCA	900
MMCSSAARNS	ANMCNCTCYC	CKCTKTGKTK	AAAAAGNAYW	CCCCMAAATT	TYTAWTTSSC	960
CCSCGCGGGN	CCCNCTNTTT	TSCNMTWCTM	WNYTNCRMCC	MMMSNCKSNG	KKGGNRCNN	1020
CRCCSNCCCM	AAWYNTKGYN	KNTATMAGC				1049

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTCGGCAC	GAGGGAATCG	AGAATCCCGG	AATGGTGAAG	CCTCGGTGCC	TGCCGTTACG	60
CCAAGAKTCA	GGGTGAGCGG	CCCCCGGTG	GGAATGCTGA	SGCCAACCGG	GAAAAGGGTG	120
AGGGCTGGGG	TGGAATAACT	GAANGTTACT	GGGATGGAAA	ACCCGGTATT	GATATGTATT	180
GGGCCGATCA	ANGTTGTGGG	AATGGGGGAA	GGCTGAGGGC	GACCTGTTGG	ATTTGGGGAA	240
TTGTYRTGGA	CRACACWGGC	CAGCCMGCGT	GATGGTTTGG	T TSAANTTTT	GTGCCGSCCA	300
CANGGTGATG	GGATTGATTT	TGATGGGGCC	SATCGAAATA	TTGGGTATGC	CNACGCCSAA	360
CGAGATYGCC	GGGACGTTCA	TGGGCGGGAC	AACCMASGGT	CCSANGTAAK	GGTTTCCTTN	420
ATNTTGATCG	GGATTCCGGA	ACTMTSTCGA	TGSGCTCSAY	MTSATSGCCC	NACNCCWCCG	480
YTTATTTTMS	GCTNAYGGGA	ATBAMRGGAA	CAAYNTCCCT	CCCMGGAAAA	ACCAACMSGC	540
CCTGGTNSYC	CNCCCRCCNC	AKAACCCRTT	KCTGTRSTMC	CCSMAAATNA	CSCCSCCTTS	600
NACTCCNCSG	AANTNSCCCC	CCCSCKNNTT	ATSTYCCCGK	GTTCCCCCMC	CCCTTNAAMC	660
TCCCCGGTTA	ACCCCCWTNT	SNCNCCCCCS	YTAAKMNCRG	GCTTSTTNCT	CCCCCYTRMK	720
CNCCCCCTCK	SAMCWNCNC	CTCKAACNAC	CCCKCYK GSM	TNCCCAATNT	WCMWCKCCNS	780
KTTNTMCTKC	CCAAYTNCRC	CCNCRCTCCC	CCKSTSTCAM	WTATAAAACC	WCWYAWYNNK	840
KCNCWMAWTA	MGACWCTCNY	NCCCCNCNCK	NTTKTAMWCC	CKMCCCKCSW	TWCYCKCSCC	900
CCMTCTMNAC	YCCCCCKKTY	NKWMCCCTTC	CCCCCTCCC	MCNMBMKTCT	YCSGKTWCWC	960
NCYNTTMTCN	CYNANMCKCK	KTCTCTTCN	CRNTCTCCCC	CCWCCCCCV	KKCTCTSKCC	1020
CNCNCTCCSC	MMKGSC					1036

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AATTCGGCAC	GAGATCATGA	ATAGCGGGCT	GGTCAGCACC	GAAGTGGTCG	GCGATCTCGC	60
GAGCAAGTCT	CGTCTGCTCG	CCCAGCAGGA	GGTCGGCATC	GATGCGGACA	CCTGCGATGT	120
CTTGGATGGT	GTTCAAGTGC	AGGTAAGGCC	GACGCCGCAG	CTTTGCTAGC	AGGGTGTCTT	180
GGCTCTTCGC	ACGTGAGGTA	ACCAATAACT	CCGACGCAGA	CCAAC TCCGG	CCCTCGATCC	240
GGGTACCAGG	CTCCGCCGGA	GCCAGCCGTT	GTGCCCCCTG	GGCCGAAGGT	CAGCTGCTGT	300
GCGATCGAAG	TAAGAAACCG	CGCCATGCCC	GTCGCCAAGT	ACGACTGACC	GAGCAAACGA	360
ACGATCGTGG	TCCTTTGGGT	GGGGGTAATC	GANCCCCAGCA	ACCGCACGAG	CCACCAATCA	420
TTGGGATTTCG	GCCACTGACC	GACCAACCGC	CTGTGCGACA	CCCCAGCGGA	ATTGGTGGTC	480
TTCCGCGGGG	CCGCNAACGG	AATCANCGSG	ACGCGCTCGC	CGAASCANCC	GCATANCCNT	540
ACATANCAAC	GGNNTCTGCG	CCCACATTTT	GGGSTTMTGC	CCCTCNGCAA	CSSNAAYNCC	600
CCCAATTCYG	AACNAAAAAA	TTGGYCCATY	ARNGTYCTCM	CCAAAAACCN	AWTCCCCKTA	660
TCCCCCGGGG	GGGRCCCCYY	NMNAAAACGG	CCCWWAANCC	CCSGGGCSCC	CGGGTTRWTN	720
CCCCTTGTCT	GCCCNCCSGG	TTTGGTCMCM	GGSCMMTNWN	GGGNTGCSCC	CCNCNAAAA	780
AAAAAYCKNG	NCAAATYAAA	CCCKYCMAAA	ASKTGGGSSC	CCCMARCCGG	GGKAAKKWWA	840
ANTTAANCCN	KAAAAAAWW	NCANNMCCCC	NGGGNCCCTAA	GGKYTTAGGG	GTTSTTNANG	900
ARAAAATMTC	CANATMNSSK	TTNNAAAAAA	ASCCSWAKCC	CCCNNNKKNN	CCAAWKAARR	960
SRCCTTCGGG	TNWNSSGGGG	KKKKKTNCMS	KMNMMTTWGR	CCCNCCGCCN	NNTWKCCCTN	1020
TCCNYGGNGC	RNCAGN					1036

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATTCGGCAC	GAGTCGATTG	GATCGAACAC	GCCCCGACCT	GGCCAGGCCA	CATGGGCGCG	60
GCCATGGCCA	ACGCCTACTC	GGCCAACCCG	AATCCATTCT	GCGTCTCACC	GCAACCCCCG	120
AAACCGGCGA	CCGCGGCATG	GATCAACCCG	CCCACCCAG	ATCCGAAATA	GCGTCCACAT	180
AATGAGACAC	TGGCGCAAAG	AGCTTGACAG	GCGCCGCACC	ACGCAAGCTG	TTAGACGTGT	240
CGGTCTTGCA	AGAAGCGGGT	TGGCCACCCA	AGATCACGCC	GCCCAAGGGC	ATCGAGTCAA	300
CGTTGCGGTG	GTATCGCGCT	AACGTCGGCG	CCGCCAAGAA	ATGACGGTGC	GCATTACCAT	360
GGCCCTGCTG	ATCACCTTTG	GCCACCTGCG	CACCANAAC	ATGANAGCC	TTATGCCGAG	420
TCTCGTGGAC	ATCGGCAGCC	GCTTCAAAAA	CTCCTTGTCG	ACAATSGTAT	TGCTGANCCG	480
CCGAATTCTT	NTRCTTGCAA	SAACACTNCA	TGTTNCSGGT	NAACAACCYT	GGTTNGAAAA	540
ACANCCAATA	TTGAANTCCC	ANTCGGGCAM	GAACNGTTM	CGGAAGKTGK	TGGGAACGAA	600
TGKTGCCCAA	AAATCCCGGG	NGGTRAAAW	CCCNATATGG	MSAATTTTSC	CTNGAACAA	660
AAAAGGTCCA	AGKYCAAAGG	NGCCCCCCCC	SGNAAATTGG	TGAACSCAKA	WYANRTTCCC	720
WWWTNCAAA	MTTNGGGTCC	KNNTCCCCWT	AAANGGGSCN	CCCCNCCRG	GMGTYTCCCC	780
NWNMGGGMGN	CYYCSCCCCA	AAAAAAAMMM	MTTTCGKGG	SMGGKKCCCC	CCSGGTYWGG	840
GKKYTTAAAC	CCGGKGGGTN	CAAAAAANAN	ACCCCCCAMS	NGGGGGGAAA	ATTTGNAAWT	900

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AAGGKKKTKC	SCMACCCCAA	AAANMMNNCN	AWNCCCGMGK	SARGGGGRNY	TTMKAGGGMG	960
GNYYYYCCCW	YCGGGGGGNA	NAAYAAAAGK	NGSNGRGAAT	NTTNTTTTGK	RSSSRNKTIT	1020
TYNTCCTYCN	CCNMGNRWG	SRAMNTGKTS	NSSGGGSGGC			1060

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTCGGCAC	GAGCTTCACC	AAAGAGCTGA	CATGCCGGGT	GATGCGACAT	CGCATCGAGG	60
GCAATACGGG	CATGGATGAN	CCGAANGGAN	TCTGGCGTTC	GCTCAACTGG	ATTACGGTTC	120
CCAAGGTGAA	ACGCTTTGCG	GCGAAAGATG	CGACGCTTAA	CTTGCGCTTC	CACCGTGCAA	180
TGTTNGTATG	GATGCTGGAA	CCGCGCTGAC	NGATAANGAA	TTGCTGGTTC	GCCGGGCACN	240
ATGGATGGTC	CKSTTTTCNC	TCCGCSGTTA	AATTGCSTGT	GCATCATCTG	GCAGGCTATG	300
TTCCCGCTAC	RCTGCAGCCC	ATCATGGATG	TGCGGCTAAC	GAANAAGTTA	TGACATGGCG	360
CAAGCGAMTC	GGGCATSCNC	GCGGCAMTTT	CGCAACCTGC	TGTGTNTGAA	GCGTMTCAAC	420
CGAATGCGGC	GCTYAAAAGC	NGGCTTGCGT	TGATTMMAAC	CNAACCCNTN	CNATYCTTTG	480
CCGNGNMNTG	CGTTCCTCTCC	AACTCCGKKG	SYTGCCNCCG	TGAAACCCMA	CTNCCCCCCC	540
GTTGGACTTA	MRTNTTCAAA	AAMCGGMTNA	ACCSGAATNN	SAACCTNCCR	TCAAANTAMM	600
SAANTCGGGC	TTYGGGNRCC	CCCCNGAAYW	TTCKNCNGGG	GMNNTYCTCN	GGTTYNGGCG	660
SAAACNTTTG	CCRTNCYMN	TTTACAMGGC	NCMTNMTTGM	GGGSCSNNAS	GWCCCGGGKK	720
TNTTTNCAAW	TCNCNSKTTT	TTKGGGGGGG	GGCYGRTRMC	NCGGGCCCCC	GGCCCKKMAA	780
AAAAAMCMSA	RRCNCYGGG	KKCCCCCCCC	NNATNGGGCG	YKCRAAACAA	ACCCCAANRA	840
TNGNGMGGGC	SMACCSGN	GYNAAAKGGT	TSNSCTMANM	MKGMANNNCT	SGMSCCMNSN	900
NCTGMGGGKT	TTKGNNGAR	AANAMKMGGM	RCGGNCGCNN	GAAAGGGSMS	GSCKSCNNGN	960
NGASNGWMGN	CRNNGANRCC	NCNGYGNMRN	NNGNNNGNNN	GGGRKNNACN	NMKMCAWSMC	1020
NSNMMGNNS	CGYMTNKGCG					1040

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTCGGCAC	GAGACAANGG	CGTGAAATGG	GATCCGGCCG	AGCTGGGGCC	CGTCGTCAGC	60
GACCTGTTGG	CCAAGTCGCG	GCCGCCGGTT	CCGGTCTATG	GGGCCTAGTT	ATCTGCGCCG	120
AGCGTGAAC	TTCGGGCGAG	TTTCGGCCGT	TTTCTCGCCC	TGGCTTCACG	TTGCGCGAAG	180
TKGGGAACGG	TCAGGGTTCG	CAAACCACGA	TCGGGATCGT	GCGGTCGGTC	CAGGACTGGT	240
ANTCCTGATA	CTTKGGTACA	TCGTGACCAA	CTGTGGNCAA	TATTCGGCGC	GCTCCTCGTC	300
NGTCGCGTCC	CGCGCGGTAA	GGTCCANCA	TTCTTTTTTC	TCGTGCCG		348

(2) INFORMATION FOR SEQ ID NO:314:

10084343 "022502

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AATTCGGCAC	GAGAGACCGG	GTCGTTGACC	AACGGACGCT	TGGGCGCGGG	CCCCTTGCGT	60
GGCATCAGCC	CTTCTCCTTC	TTAGCGCCGT	AACGGCTGCG	TGCCTGTTTG	CGGTTCTTGA	120
CACCTGCGT	ATCCAGCGAA	CCGCGGATGA	TCTTGTAGCG	CACACCAGGC	AGGTCCTTCA	180
CCCGGCCGCC	GCGCACCAGC	ACCATCGAGT	GCTCCTGCAG	GTTGTGGCCC	TCGCCGGGAA	240
TGTACGCCGT	GACCTCGAAC	TGACTCGTCA	CTTCAGSEGG	GCAACCTTCC	GAAGCGCGGA	300
GTTCGGCTTC	TTCGGAGTGG	TGGCTCGTGC	CG			332

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

AATTCGGCAC	RAGTCGGTCT	AGACGGATTC	AATGCTCCCG	CGAGCACCTC	GCCACTGCAC	60
ACCCTGCAGC	AAAATGTGCT	CAATGTGGTG	AACGAGCCCT	TCCAGACGCT	CACCGGCCGC	120
CCGCTGATCG	GCAACGGCGC	CAACGGGACT	CCTGGAACCG	GGGCTGACGC	GGGGCCGGCG	180
GGTGGCTGTT	CGGCAACGGC	GGCAACGGCG	GGTCCGGGGC	GAACGGAACC	AACGGCGGGG	240
ACGTGGGGAC	GCGCCCGGCG	GGATTTCTTC	GCACCGGSGC	ACCGGCGGGG	CCGGCGGCGT	300
CGCACAACGG	CACCGGCGGG	GACGCNGCGC	CCGTNGGGCG	GCTTCTKGAT	GGGCTCCGGC	360
GGTNACGCGG	CACGGCGGCG	CCCGGCTCAC	CGCCNGTTGG	GACGCGGGGA	CGCGTNACCC	420
CGATCTTCTT	CCGCNCCCCG	GAAACCGCGG	GGCCGGCCCC	ACATTAKACC	CGGCGGNACC	480
GCGGMCCCGG	CGGAACGGNG	GGYNTTTTCC	AACGGCGGGG	CCGCGGAACC	GNMGGSTGTT	540
CCTTNGGSGA	AGGNCCAAKT	CCCGKCTANC	YYAATCCCCG	ANGGKTGAMC	CTSATGSNCA	600
MYTTMAGGAA	CYTNNCCANT	KTTSGRACCW	CRCCNGGAAA	ASRAWNKNGT	KGGCAAACNA	660
NNTNICYTTKN	NATTKGGNNA	AAAANCCCTY	CCWCSGRACT	NCCCCCNGM	GRGMCNNTNN	720
NTTTYGNCCNN	CCCGGSNAAM	RNTTKATTTT	NGGGGGNTCN	GGGTKMNNNA	AACCCCAAAM	780
MNRNNKSCA	ANGGGSNGC	NKNNMMNSGT	TTYCKNMRA	MRNWTYKNKN	NTCNGARSRN	840
NAAMCNSNK	NGKKKNKAA	ARNNTTWKTN	KNSCNNNCNN	GRRNGVRGGC	CKMKGSNMNG	900
MCWHNAWRNG	NNGSNCNCKC	NNKMNAAAA	AASGGVNCKS	NSMKNKKKKG	NRGGGGGGGG	960
GG						962

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCGGCAC	RAGAAGACGC	CCGAANGTTT	GCGCTGGCTC	TACAACTTCA	TCAARGCGCA	60
GGGGGAACGC	AACTTCGGCA	AGATCTACGT	TCGCTTCCCC	GAAGCGGTCT	CGATGCGCCA	120
GTACCTCGGC	GCACCGCACG	GCGAGCTGAC	CCAGGATCCG	GCCGCGAAAC	GGCTTGCGTT	180
GCAGAAGATG	TCGTTGAGG	TGGCCTGGAG	GATTTTGCAN	GCGACGCCNG	TGACCGCGAC	240
GGGTTTKGTG	TCCGCACTGC	TGCTCACCAC	CCGCGGCACC	GCGTTGACCT	CGACCAGCTG	300
CACCACTCGT	GCCGCTCGTG	CCG				323

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AATTCGCAGT	GTGTGTGGCG	GCGTCCAGAA	GAAGATGATC	GCGAACATCG	CCAGCGCCGG	60
CCAGGCTATG	GTGCCGGTGA	TGGCCGACCA	GCCGATCATC	ACCGGCATAC	AGCCGGCCGC	120
CCCACCCAC	ACCACGTTCT	GTGACGTGCG	TCGCTTGAGC	CAAAGCGTGT	AGACRAACAC	180
ATAAAACGCG	ACGGTGACCA	GGGCCAGCAC	CCCCGCCAGC	AGGTTCGTGG	CGCACCATAG	240
CCAGAAGAAC	GAGATCACCG	TCNACGTCAC	CCGAGTGCCA	ACGCGTTTCG	GGTCGGCACC	300
GCTTCCCGCG	CCAAGGGCCG	GCGCGCGGTT	CGCTTCATCA	CCTTGTCGAT	ATCGGCGTCG	360
GCNACCAGTT	GAGCGTGTTG	GCGCCGCGCG	CSGCCATCAT	CCCGCCGACN	ANCGTGTTGA	420
GCATGANCA	GCGATGAATG	GCGCCGCGGC	TCGTGCCGCT	CGTGCCGAAT	TCAACTCCGT	480
CNACAACCTG	CGGNCGCACT	CGAACCCGGG	TGAATGAWTG	AATTTAAACC	GSTSAACANT	540
AACTACATAA	CCCTTGGGGG	CTCTTAACCG	GTYYTGAANG	GGTTTTTTGC	TTAAAGGAAG	600
AACYATTTCC	GGATANCTGG	CSTTNWTARC	GAAAAGGCC	CRCCCATNGC	CCTCCACAGT	660
TTSCCCCTGA	ATGGSAAATG	MNCNCCYKNR	CNGGGNCTTT	AACRCSGGCG	GGNTTTTGKT	720
MCCCNCTKA	CNTTMMMTGC	ARNNCNGGCC	SKCCCTTCK	TNTYCCCTCC	NTCCCCCNST	780
TNCNGKTCCC	CNNAMNYTNW	ACGGGGGGCC	YTNGGGKCRM	TWTKKTTTGG	GCCCCMCCCC	840
MAAANASAA	GGGGKRNQTY	CSTTTGGCNC	CCCAMAARGG	NYCCCCCAM	YTNRRKMCSY	900
CNNTNKGGNN	CTGTNCKNCG	GAARAMAMCC	KCCCCGNSTS	STTNGTYWAG	GNRWKGNRSG	960
CCSCCCCGGY	MNNNAAYAWN	WMNATNCNNS	STNANMAKKN	NNNNNNNSCN	WNGNGNNTCN	1020
SCNSNGGKBC	CSCC					1034

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

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AATTCGGCAC	GAGCCCACAT	CCGGGGCCGC	TCGTTGCATG	ACTCGTTCGT	CATCGTCGAC	60
RAGGCACAGT	CGCTGGAGCG	CAATGTGTTG	CTGACCGTGC	TGTCCCGGTT	GGGGACCGGT	120
TCCCGGGTGG	TGTTGACCCA	CGACATCGCC	CAGCGCGACA	ACCTGCGGGT	CGGCCGCCAC	180
GACGGGTTCG	CGCGGTGATC	GAGAAGCTCA	AAGGTCATCC	GTTGTTTCGCC	CACATCACCT	240
TGCTGCGCAG	TGAGCGCTCG	CCGATCGCCG	CGCTGGTCAC	GAGATGCTCG	ANGAGATCAC	300
CGGGCCGCGC	TGAGTGCGCC	TCCCGCGAGC	A			331

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

AATTCGGCAC	GAGATCGTCA	CCCTGGCGAC	CAGTGCACCC	AGGCCACGCC	ACCAGTTACG	60
GCTGATGGGC	CAGAAATG	ACCAGGTGCT	GCCCCATCCG	CCCACCGCAC	TGCAGCTGAG	120
CACCGGGATC	GCGGTCCTCA	GCTACGGCGA	TRAGCTGGTG	TTCGGCATCA	CCGCTGACTA	180
TGACGCCGCG	TCCGAAATG	AGCAGCTGGT	CAACGGTATC	GAAGTGGGTG	TGGCGCGTCT	240
GGTGGCGCTC	ANCGACAATT	CCGTGCTGCT	GTTTACAAGG	ATCGGCSTAA	GCGTTCATCC	300
CGCGCACTCC	CCANCGCCGC	GCGGCSGGGG	CGGCCCTCTG	TGCCGACCGC	CCGAGCGCGT	360
CACTGACGCC	ATCTCCGTCG	GCGTTAACCC	CGTGAGAAGG	TGGGTCGTGC	GCAAGTTGGG	420
CCCGGTCAAC	ATCNATCCGC	GCCGCCATGA	CGCNGTGCTG	TCCACACCA	CNTSNGACNC	480
CCCCCAGGAA	CTGGTCCGGC	AMTNCAGGAA	NTYCGTGTGG	GCACCNGCTT	CTTCCGKTRT	540
GGCYTAAACT	TCCNATSTTN	CSGCSGGCCT	CTGGCGTTNC	GNCCGGGGCCG	NTCTTNCCAA	600
ATCGGSMMAA	ATCCCCANMC	AAACCCCCCG	GGTCTTGSGG	GCSGGGNGGC	GGCCNAWNCC	660
AAACCCCCCC	NTTAAANTCT	TTGKTNCCNN	CNCSGGCNCC	NCNAANSCAN	CCCTTTKGGC	720
NCTTCCCCCC	CCCAWTTTAA	CCGAKCGSCN	AAYCCCAAGY	TMMGKCCYCY	KNAAAAA	780
AATTTGSCSG	CCCCAANTAA	ATTCCCNNGC	CCYTTGGGGG	CGRANCNYNT	TTTMCCSNSS	840
TKGNNNNAAMC	NGGANCCSGG	KAAYTMMTKG	NAAYCGCCSN	AAMBNTTTTC	TAANNCCCN	900
YNCCCSGAAA	ATTNNAMAAM	CMNNKTGSNG	GGGGKTTSNC	SGKKGRAGGM	AAAAAANRSN	960
SKTTNMCNNN	SANMNCNSNN	SGGNSNNNNN	NNNCNCGYKC	CSNAANMCCC	CGCGGGGGGG	1020
CCMMCC						1026

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

AATTCGGCAC	GAGAAGACGC	CCGARNGTST	GCGCTGGCTC	TACAACTTCA	TCAARGCGCA	60
NGGGGAACGC	AACTTCGGCA	AGATCTACGT	TCGCTTCCCC	GAAGCGGTCT	CGATGCGCCA	120
GTACCTCGGC	GCACCGCACG	GCGAGCTGAC	CCAGGATCCG	GCCGCGAAAC	GGCTTGCGTT	180
GCAGAAAGATG	TCGTTTCGAGG	TGGCCTGGAN	GATTTTGCAN	GCGACGCCNG	TNACCGCGAC	240
GGGTTTKGTG	TCCGCACTGC	TGCTCACCAC	CCGCSGCACC	GCGTTGACGC	TCGACCAGCT	300

GCACCACTCG TGCCGCTCGT GCCG

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(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

AATTCGGCAC	GANGCGTGCC	GCTNAACACC	AGCCCGCGGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGCCGC	CGGTGGCGTC	GTTGCTCTCC	TGACGGGGCG	CGGCGACCAT	AAGGTCGCTM	120
ATGCCCAGGT	AGCGGCCAG	GTGCATGGAG	TCGATGATGA	TGCGACTCTC	CAGCTCGCCG	180
ACCGGGAGCT	TGGCATCGGG	CCTGATCAGC	CAGGACGCGT	AGGACAAAGTC	GATCGAATGC	240
ATAGTGGCCT	CCAGAGTGGC	CGTGCAAMTT	CNGCGTGCTC	CACGGCAAAT	GCCTTGATTT	300
CTACTCCGCG	TANTGTTCCC	GCATCGCCTG	CGGGATGAAT	GGGAACCGCA	SGATGGCGAC	360
GAACGGGTCT	GANCTCAGGT	TTGCCGCTTT	GCGCACAGTG	GTCNACANCC	GGTACTCGGC	420
ATANATCTGG	CCCNAAATCG	GCGCCGACGG	CGCCACNAT	AANAACGGGC	ACNACAATCG	480
CCGCCCCGGT	CACCCNAACA	ACANCTTGSC	ATCGGATTTT	GTCCCCANCG	CTCAANCCGT	540
CCCGAACGCC	TCNTCCGGCG	NACTTTTCTT	NNAWTAATG	CCGCTTCCGK	CCCTGGNGCA	600
WTAAATGGGA	AACCCTTNCC	CCACCTTGAA	GGGGTTGTTG	NATTTTTACT	GSTAACCCCG	660
AATTNTTCCG	GANTCGGTCT	KCCGGGSTTT	YSTNTTCCCC	ACCTTNGNAN	GGGCCGGCCA	720
AGSTTTTCTT	SYTGAAGGGG	GAAACCCAAC	TTTNTYTYYN	AACCSCMNAA	MYMTTTYCSG	780
MNAASCCNKT	CCCCTTTAAC	CAMGSGGTN	AACCGKTMNG	NGGKTAAAAA	GGGSKNNKTG	840
NCCCCYMANG	GGGGGAAAA	TSTKTCNNCG	GGGCCKAAAW	ACMMMMYGN	GTGKKKNKSS	900
GCSAAATTTT	NMMRAACTKN	GGGGCCSSGA	NNTTTNAAAG	MSCCCCCSNN	GSTGKCCCN	960
NTTTCNNAA	WMKKGKNWNM	SNMNSCSNGG	GKYNSSGSNN	NNAAGMGGGG		1010

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

AATTCGGCAC	GANGCGTGCC	GCTNAACACC	AGCCCGCGGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGCCGC	CGGTGGCGTC	GTTGCTCTCC	TGACGGGGCG	CGGCGACCAT	AAGGTCGCTM	120
ATGCCCAGGT	AGCGGCCAG	GTGCATGGAG	TCGATGATGA	TGCGACTCTC	CAGCTCGCCG	180
ACCGGGAGCT	TGGCATCGGG	CCTGATCAGC	CAGGACGCGT	AGGACAAAGTC	GATCGAATGC	240
ATAGTGGCCT	CCAGAGTGGC	CGTGCAAMTT	CNGCGTGCTC	CACGGCAAAT	GCCTTGATTT	300
CTACTCCGCG	TANTGTTCCC	GCATCGCCTG	CGGGATGAAT	GGGAACCGCA	SGATGGCGAC	360
GAACGGGTCT	GANCTCAGGT	TTGCCGCTTT	GCGCACAGTG	GTCNACANCC	GGTACTCGGC	420
ATANATCTGG	CCCNAAATCG	GCGCCGACGG	CGCCACNAT	AANAACGGGC	ACNACAATCG	480
CCGCCCCGGT	CACCCNAACA	ACANCTTGSC	ATCGGATTTT	GTCCCCANCG	CTCAANCCGT	540
CCCGAACGCC	TCNTCCGGCG	NACTTTTCTT	NNAWTAATG	CCGCTTCCGK	CCCTGGNGCA	600
WTAAATGGGA	AACCCTTNCC	CCACCTTGAA	GGGGTTGTTG	NATTTTTACT	GSTAACCCCG	660

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AATTNTTCCG	GANTCGGTCN	KCCGGGSTTT	YSTNTTCCCC	ACCTTNGNAN	GGGCCGGCCA	720
AGSTTTTCTT	SYTGAAGGGG	GAAACCCAAC	TTTNTYTYYN	AACCSCMNAA	MYMTTTYCSG	780
MNAASCCNKT	CCCCTTTAAC	CAMGGSGGTN	AACCGKTMNG	NGGKTAAAAA	GGGSKNNKTG	840
NCCCCYMANG	GGGGGRAAAA	TSTKTCNNCG	GGGCCKAAAW	ACMMMMYGN	GTGKKKNKSS	900
GCSAAATTTT	NMMRAACTKN	GGGGCCSSGA	NNTTTNAAAG	MSCCCCCSNN	GSTGKCCCN	960
NTTTCNNAA	WMKKGKNWNM	SNMNSCSNGG	GKYNSSGSNN	NNAAGMGGGG		1010

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

NGNGGGGWNS	NTCAYCAYCA	YCACSGGGYW	CWATTGCGGC	CGCAWCTTGT	MAASAGATCT	60
CGAAYTCGGC	AMGAGGGAMT	CKCTMGCNCC	GCTGTGCAAN	CCAATRAGGC	CTRATAATTY	120
CCACTCCACA	AAAAACCGTT	GTGTGTAYYT	SCCGRAAATR	AAGGCGCCGG	TNTCAACWYC	180
GCCGGTKTTY	CCRATYCCCG	TKTTGTAMCT	GCKKGGGTSR	AAAYCCCCGG	TGTTGGAYCC	240
CCGGATTGAA	ACTGCCGGKT	TGAAACTGCC	GKTTTSGCSA	TCCGGKWATT	GAMSTCRCGG	300
ATTAAAAAAC	CGGKKTGGN	GCTGSNCGTG	CCAAATNCGR	AYCCRATAYC	CCATGGCCTG	360
KYCTYCTCCK	YCGGTACCCA	AAYCTGGGTA	TCCTATACTG	GYCCCTAAAK	GCAAWYCKGG	420
GCTGYCMMTK	TTGCKGGSgt	CCNAATTTAS	CACCASCGGT	TCCTTCCATA	CCNAAACNCG	480
CKTGGGCWCC	AGMCCGRAAA	AAAKAATAAT	RAKAAKGGTG	CATNYCCAAA	ACCNCCGCCN	540
CCCNANTNCN	ATCCGNTNCC	MSCNCCCCCA	GCGGTNAAGK	TKSGGAAYTT	CTMMAACCCC	600
CAAANCCCCA	TAACNTNCGR	GAASAAACCC	CTYCNCGGGG	GYCNWNCAAA	ACASCNTTAT	660
TTGCTKSTTT	CGGGMWCCGT	GCCGCCNAAA	YCCCAAATA	CTTTYTGCGT	CCNAGAKAAA	720
ACCNCGGGCN	CCMCCCSNAA	NWTATYTCTT	KGGCAANCCC	CSAAACCTTR	TCMNACCNC	780
ATRMTCCTT	CCCCVSCAAT	TGGYCGGRAT	NCGSNCCYTY	TCAAARKKSC	CAKWWNNGNG	840
GRRNNACCM	ACCCCAAGTY	CCMNAATAATN	GKCCCCGCTC	CNAACACGNK	TYYTCCSAAA	900
ASCCCWCCCC	CCCCCCCRAA	AACCCCCCNA	RKANTNCCCCA	AAAACNYNGK	GGCCCCCCCC	960
CAAACMAAAA	AMCCCCCSGM	RMACSGGGGN	NMCCCCGKKK	KKTTTTCTTT	TKCCMRSCCC	1020
AAMGCAMWSY	KSKTNMAAAA	GGAAGRANCN	TYCCSANANM	TCCCNWRSW	CCGSWGMGNA	1080
GAASMCCCC	CS					1092

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GGGGGGGNNN	NATACATCWT	CYGTGYACCG	GGGMTCTAKT	GGCGGGCCGC	AATCTNGTCA	60
ASAGATCTCT	NAMTTCGGGC	ACAAAACTW	GACAAASYMT	CGNGCNMTCC	GTGTCCNTKA	120
TCGCAAAACG	NGTRACASAC	ASACACRTAT	GTGTGCCCCAC	CASCAAYTCK	TTGGGACCTC	180
GCTRACCGGY	TGCCCRNACG	CCACGYTGCS	CWTCTATCCC	RACGCCGGCC	ACGGGYGGGG	240

ATATTCCAGG	CACCACGCC	AGTTTGGTGG	ACAATGCCCT	GGCAKTTTCC	TCRAANTTCG	300
TGAAACCGAA	TTCNSMTTGA	ACCNCCAARG	CCCCSNCCNR	AACARTTGGG	WTCCGCGGTT	360
CTCCCCACCG	KTTTCCGGGG	GTNTCGGCAN	AANCGCACCC	WTGGWTTCTM	TCNCCGCACC	420
GGGCGGACAA	NTCGGGTTGC	AATTTTGCRA	AYCGGGGCCG	GGATTCCSCA	AACGGGTGCC	480
GAAACTGTTY	YCRAAMACCG	GGAKCCGCAA	TTTCCGGGCR	ANAAATTTCN	YCNCACCACT	540
GCTTRTACTT	CCCCGACCGT	AACMANTTTC	ATCGTCNTNN	CCTCTGCCT	TGGGGCAGGG	600
CKAAAYACCG	CMTTKGGTTT	CGCAACCTGC	GGCCCAANTC	CCNAMCCRCA	CTTTCNATTT	660
GGNTCGAATT	SCCCCCCGGT	RANAACCSCC	NTGGCCNNYT	CGGASSAAAA	NGGGCCCTNT	720
KGGCNSCCCC	AGTAANACCC	TACCNAYTS	CAWTCTTTGC	CAAASTTKGG	ACGAANSKTG	780
GGNTTCCGGK	ATTTYTTTGS	GGNCNCCCTN	TATNGGSNTN	GGGCKCYNC	NCSTKTGKCA	840
NASSKAYCCS	NGNKGGGGGT	ACCCCCCTMG	GGGGGTTTTT	NSSGCCCCCC	AWAYGNKSTG	900
GCCCCCNNGG	GGAACAATWT	MWWTMCNSGG	GGGAAWTTTT	NTSTGGAMCS	SGGACYCCCR	960
GGGGGKTTTT	TCCCCCNCSA	NNAWANGGGG	GGGGGANAYT	NTGNSGNNGG	KWNTTTATTT	1020
YTYCYCCTM	TKACMSGGGG	GTTTKKAKNG	GGGGGAGAAA	ANAAAAAANA	RAKGGYKNTT	1080
TSKNACNCT	GKWNWNWANR	NAGAGKTCCT	CKCKCCNCSG	SNTTCTTTTT	MGNSGSYGGG	1140
GNNGNNNAAA	ACNKSRRMAC	KCSYTYCCCG	CGYCTCCTCC	NCNGGGGYGS	NGSCGNSTYN	1200
GNNKGRKWT	TNTMGNCGTN	SCCTCCNCCC	GCKNKNTGTC	TMTCNMYGSG	C	1251

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

AAYTCGGCAC	MGAGTATCAC	CAAKCTGYGT	GGCCCAGCAA	AGTGGAGCTA	TTACTACCTG	60
TATGTGATCC	TCRACATCTY	CTCCCGCTAC	KTGGTCGGGT	GGATGGTGGC	CTCGCKTGAK	120
TCRAAGGTCT	TGGCCRAACG	GCTGATCGCG	CAAACCCTTG	CGCCCAGCAC	ATCAKCGCCG	180
AACAGCTGAC	CTGCMCGCCG	ACCGGGGGYC	GNCAATAACT	CCAAACCGGT	GGCMCTGCTG	240
CTGGCCNACY	CCGTGTCCCA	ANTCGAACTC	ASCCSGCNMA	CCAKMAACKA	NAACCGTTGT	300
CTGAAGCCCA	GTTCAAAAAC	CTCAAGTWCC	GGCCCRACNT	CCCGAAACGG	TNCGAGTCKA	360
TCSRAGSGSG	CCGGGTGCMC	TGCAACCGGT	TCTTCGNTG	GTRCAMCCCN	AAAMCAAGCA	420
TTCCGGGMTC	CGMMTGCCCA	CGCCGCCAAS	TTTMCCTACG	GCSGSCCNAT	CAAATTTCGCC	480
GGGAACSGSN	CCMCKCTCNK	GGAMACGCCC	TWCCAAAACC	CYCGAACGGK	ATCCTTCKGY	540
NAACNCCCGA	RCNCCCKSKT	TCCGGGCTTC	NMSGCGAATA	CCCKNSCMNT	CCGAATCCAA	600
TTCCCMKYGG	CTTTTYYYCC	CCCCGGCCCC	AAAYNGGGYC	CCTASSNMKC	KNCCAMNANT	660
CCNWATCTGG	NGGTCCCNAN	KYYGGCGTTC	NMAATSAMNA	NMNRGGGTYT	TSCYACCMN	720
AACCGKNNKG	KCCCCMKCTK	MANAAAKATT	RATCAMKWNG	GGNKCKCNCN	NAAMACCSCN	780
CNCYNCWYTC	TMYCSSKWGC	GCSMYNANCA	SNGGGGAGGW	GGSGRMKMCT	CTMTCTCNCT	840
MGCGCCKNTN	TYCKSGAKAT	ACASMNKTCC	GCGCNGCGCN	MAAMANRAKA	CTAKCCGYGN	900
CCSNSTMTYN	CTSNNMKMNN	TCCWMWNATC	NTYYGKKCNN	KCTMKATNWC	CSCTSKCNCK	960
MRAMTCKTYG	SNMTCCTCCA	TCNCTCKKSC	SNMSKNTCKC	KSCNCCNCWN	CNKCNMKCWN	1020
GGNSTCRCCY	TCTMNNNTCS	AGCKCGSKNC	WACNCACACK	NGWCTYTTCC	WKNNMKCNKM	1080
TCKCKCACRG	MTMTCWCCS					1099

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GNGNTATACA	TCWCTGTGYA	CCSAGGATCW	ANTGCGGCCG	MAAKCTWSTM	CASAGATCTC	60
AAAYTCTGCA	MGAGCGGCAC	AKAKYSTCGT	CCMRACCCGG	CAYACWCCWG	CNCGCCCCWT	120
CTTRGACCGG	GGCKATASMC	ACCGTTGGCC	CCGGCNCGCA	CCTACACCAC	CCACGCCGCC	180
AGCGCCCCCW	TRAMCAAACC	ACCCCGCKTT	TACCGCCCGC	GCCGCCGGGG	CCACCACCAG	240
CCCCACGGCG	ACCACGGGCG	CCGCCGTTGC	CAAAACAGGC	CCGCKTTTGC	CACCRA	296

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

NGNGSGNKMY	ATCATCWTTT	TGCACCSNGG	MTCWATTGCG	GCCGCAATCT	TSTMNASAGA	60
TCTCGAAYTC	GGCANGARCA	TCTGCGCGGN	GAATGTCCAA	AWGTCWKTA	CGGCMATCGG	120
TTTGCCGYCA	ACCACKCTRT	SCAKATGCGG	GCCAMWTYCA	AACCRATTAT	TTGGGYCGAG	180
AAAATTTMCG	CKTGTRASCA	ACCTGCAGCG	GGTCAASCAA	CAGCCTCTRA	ACCGTAAATY	240
CKTAGGTNKT	YCCGGCAACA	ASCYCRATAA	TSCGGCCCGC	AMCCACAAAA	CCTGANTNGT	300
TNTTCNCRAA	NCCGGTYCCC	GRAGGGGTSA	ACTGCSGTAR	GCTTNTCWYC	NCCTTRACAT	360
TAAACCCCCC	CGGNTCWTCT	CCGCGCCCAA	ATYCYTGCCC	WTKGCNACCA	YCCCANCTTG	420
CSGTATGGTS	RAANCASTSG	GCRAACGGTM	MCCSTACCKC	TGGCTGATYC	KTCGGNTCCS	480
SNAATTCGGG	GATTTACGGS	CAMGGTTAAY	CCAGGYCCCC	TNTGCTYCKY	CNACAACCSG	540
ATCMWCNCCG	TACCTKTTAA	AATTCTTTGT	GGTGGAACCC	AWYCKAAAAA	NMTNTYCCCN	600
TCCAMMGGGG	CYCGGAAKKT	CNACNTGGKT	NACCCCTNCC	YTTGAASTTT	TCYTGNNCCC	660
GGCCCKAAAS	ANACCSGAKC	CCCGGAAYCS	WTAGGCTYCN	TGCCCCSTTA	AATTGKNCYC	720
AATCCKCCAA	CGCTCCCCGG	GGTCSSCCMT	TAAAMTTCCC	CCCKSCASNG	GAATYCYKSG	780
GCWGTMAATW	CCNCCCNNTT	CYYGKNAAAC	SCCCCCWKGN	GSCTYCCCN	SNTTSSGCCS	840
GGTTSAMYC	AAAATWNGGG	MMCNRAGNCG	SGNAMCCSCN	GKKGGGSATW	TKAAYYCYGG	900
GGGGGTCNYC	CCCCRCSNAA	AAGYGTKGGC	KCCSSSCCYC	CCMARTTTYT	CNGGMRCMAM	960
ACCANGGGNG	CTCCCGTNCW	WGGCTCCCSN	SNSMAMAAAN	NKCKCKKGGG	CKGARRNMNA	1020
MCTCSNGNGG	WTCCCKNKTC	NSCNSGNCGS	YGGNSASWCC	YNYCNCCACA	ANC	1073

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

CGCCCCGTTT	TTMMMTTCAY	TCATTCACCG	GGMTCTAGTG	CGGCCGCAAK	CTTGTCKACA	60
GATCTCGAAY	TCGGCAGAS	ACAATSTCGG	GTKGGGCAAT	GTCNGGTGGG	GCAACTTTGG	120
GCTCGGRAAT	YCGGGGTAA	CGCCGGGTCT	RATGGGTSTG	GGTAATATCG	GGTTTGGTAA	180
TGCCGGCAGC	TACAATTTCG	GTTTGGCAAA	ATATGGGTGT	GGGCAATATN	GGGTYCGCTA	240
ACACCGSCAS	TGGRAATTYC	GGTATTSGGT	NACCGGTRAY	AAYCTGACCG	GGTNCGGTGG	300
TTYCAATACC	GGTAACGGGA	ATGTSGGTTS	YYYACYCCGS	GSAACGGNWW	YTTNGKTCCT	360
TMMCNCTSSM	CCKSAAMTSM	KMGSTSTYCT	MTYCNNGGAS	TAMTYNMCCC	CCGWAYCKSC	420
WAYCCCTCGT	CATYCCMCMC	SGSGYCCTCA	MNCCACCYTG	NGYYCCCTCC	MKMTCYCAYT	480
CMNTCCGGTW	CCTNTMMNCC	CSCNCRYCTC	AMCNCTKSGK	CACCNATMYC	CSACKCHTCT	540
MCYMCSCAKN	MTTCCCCTCN	CCTYTNNCCA	MCMCSTCTM	TCMAACTCKC	CCGGYCKCNC	600
MYCTCTCKCC	AYNMAACCKK	TYCYWCNWYC	YMYCKCKCAG	WYKNMCTCCW	ACTCTMYNTT	660
TCTCTCNKCC	CMKACCKNTT	CTCWCSCCC	CCACAKAYMC	YAWCMTMTCC	MCTCKACSCC	720
CYYCNYYCCM	NMCWCMTWC	TWNAKCANCN	TTCTTCTCTC	MMYMTMACKC	WCNNTCNCKK	780
SGACCYTCTC	ACTKMKCCCK	TCTCCTTMCK	CCYMWNTCC	MKYNCCCTCC	NMTCMTCKYT	840
CCTCNCNMRY	CYYYAKCAKC	NMCTCCCCAN	KMCAKCTKCT	CCCCCAKMS	ACNCKCCCWC	900
CCTCCTATCC	WCTCTCWCTY	ATCTCKCTCW	CNYCMYKMC	ACNCKCYAYT	CNACTMNMWN	960
CCANCNCTCT	CTNYCTCWCK	ACGTYCKCK	CTMCKCNMYC	NRWCTYRCCT	CKKCCNCCRN	1020
CKNMCMKCTM	CTCTCCWMKM	TCCCWCCCAT	CTMMKSTCTC	WCNMTCCCT	CNKCCYNYNT	1080
KCYTYCCMYG	CTTCKNTCMT	MCCWCCYATC	TCTMKCCTCT	CWCACYMCAC	WMTTACWNCC	1140
ACTCTCTRCW	CKCKCMCCR	MTCTCB				1166

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

NGNGGNNNT	CWTACATCWN	TCTNCACCSG	NGMTCWATTG	CGCGCCGCAW	NCTTGTMNAS	60
AGAATCTCNN	AAATCGGCAC	ANATGTCTTT	TSTMTAKTGT	GGCGGGGNGC	CACGCCKTAT	120
GTGYGCCTGG	GYTRACCCAA	CCCCGCGGCS	CGGGCCRACC	AGGCGGGGRA	TSCAGGCCGC	180
GGCGGCCGCG	GCGGYTATAT	RAAGCGCCGY	TTTTKTRATA	ACGGTSCCGC	CGCCGGGTRA	240
TTACGGGCAA	AAYCGGKTTT	TTGGGTRTAT	AACGCTAATT	GCAACCAWTT	TTTYCGGGTC	300
AAAAACYCGG	CGWGCANATC	NCGGGYCNCT	RAGGCGCATT	YMCGCCAAAA	WTNTGGGCGC	360
AAAACCCCKT	TSYTATTTTN	TGGGCTATSC	GGYTGCTTCG	GCAAACGCTY	CCCGGGTTAA	420
TCCCKTCCGC	GGCGCCGCCN	AAAAACCACC	AATYCCGYTG	GGGGTGKYCC	CMCAGGCSGT	480
TGCTYCGNGY	CACCTGGCCA	AAYYCCCAWT	AKATTGGGTG	SCYCKTSCGG	TTSYTGGGCT	540
CAATTACCCC	CNCGGGNAAA	GRRAAANAA	ATCNTCCNTT	TGCTCGGYCA	YCTTTMTTGG	600
SAAAAGGGGC	ATGGCSCGGT	TYYTTTACCT	CAAYCCCNA	NCANTWACCT	YTCCSCCCGG	660
GGGGNCANAA	CGSTTNGCTC	CGSGGNAKCC	TKGTMCCCGN	ATCNAAAGGC	CNGAATTTGG	720
TYYSSTYCNA	ATTWTWKKKY	CCCCWCNTTG	YAAAAKCCA	AAASAKCCCK	YCNCAMMYKT	780
NGGGGTYSYG	GCCKNYCTTK	SNMTTAAACC	CYCCCCAAAA	YNSGGGKKT	TCCGCYNSAT	840
KCCACCNCCK	GNGGGGGGNA	SAAAAAAAAY	TTYCCSAAA	ATCCCACCYY	TCYKTKSTRY	900
AMACCCCTT	TYMKKAYTC	CKYSCNATTC	SGMTTCWAAA	TYCCGYGGCT	TNTTCCCCCK	960
CSGGNGCCCC	AAWTTTGKTT	YCNANTTYC	CCCNAMNCM	AWTMGGGGKS	KCCATTCTGG	1020
SCYTMAANTA	AAANAANGGG	NKTTTYCTY	MANAAACACN	GTGKCNCCN	CNAAMAAASN	1080
AKMAAAKAGN	KKKMTKNNSA	AANCCNCCCC	CTSTYNTYTT	NKTNMNCKCC	CYGGKKNKGM	1140
SWSWYNTTCT	NCCCRCCCCC	YNYNKTGANA	AAMNCCYCCS	GGSTMCRNAN	ASNMTTCTCK	1200
STSTNGMGCC	KMBASNANAN	MCAMWKWYCC				1230

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(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

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NGNGGGKNNNA TMAWCWTCTC ACSSGGTCTA TGCGGCGCAW CTMGTMMAASA GATCTCNAAY      60
TCGGCAMPAN GCATMTCMMC CATATATAAC CATTGCGTCS GYWTGCAWCT CRAAWCTGTC      120
CTTCSKGGCCG TTKTACRAAG GTGGMWTGYT CWTYCCTRAA SCCCTCRATC TCKTKTATYC      180
CTKGGGCTYC ACTTTAACSG RATKSCTGCC TTKTAYCATT RATGCAAWTA WTGGYCRWT      240
KTTGCAGGCC RACGGCWYCT TTTYCCGCRA GRACAATNGA TTGGAWYCGC TYCGCRAGGC      300
CCGGCACCAR ACCGGGCNCC AAAGGYCCGC GCAAWTSCCT GGKTCAAAAAA TGGTGCAAAC      360
AAAMCNATCC CCGGYTTRAC CGCAGYTAMC ACAAKAAAAT TCCCWTGGCC GCACCAWNNT      420
TTYCRATCWY CWYCCCCACC TTRAACCTGK YTGCSGTATT GCCTKCCTGC CTCRACAGCM      480
YCNCCKTCA AACCTGCGGT GACTCCAAC TGTCTGGYCG AASGGGGGYT CAMCGGACAA      540
AACCCCRANN TCGCCAAATT TTCNCCCCC CYCGGGAAAN GKTGATMTTC TCSNAACCSA      600
CMGGGNNYTW NAACCCTGAA CSSSGSNKGA MYNSCCSGGA ANTTTTCCCT TYNGGGCGRN      660
AAANCCTTTT AAGGTACCCC KGGNGGGGKG CCCYTTGGG AAAACAACCC CKATTGGKTT      720
TGGAAATNTT TKNCCCCCA TTCNSGGGGG GGGCCCCAMC CMMCTTTTN TCMSCNMTYY      780
YCYGGGGAAT TNYTCGCCSG GAAYYCGGSM CCKGYCCTAA NCCCCMNWGG GKYSTGSNAR      840
GGRATMAWWT TYSTTTYMYC CCGGCNNCCC CCKAKMCNT KGNTGAACMA AAKCSGGGG      900
GSCNMYMWYY YCNNGNRTT TNRGSSNMT TYMAAMMAN GGGGKYWTYY CKCCNGSCNN      960
GKTYSGGGST TTTCCNTTTS GGGSSATYKG MACCCCKTMT AYCCGGGGGT NTKTKYCCCC     1020
SC                                                                    1022

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(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

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NNCNGNNKNTA TAMAYCWYCT NCACCSGGGA TCWATTGCGG CCGCAATCTT STMAASAGAT      60
CTCKAAAYTCG GCAMGANCCG CAWCTATTTG KGTGRASCGC ACCAGCGRGA CCTCGCSGKT      120
CKTTYCTTGC AGRGAGGCKK TGGGTGGCRC CGGTGGCAAT GCCAACC GCCCAAAACN      180
CCGCAAATMY CRAAAAACAA CCCSGGGGTA GKTCCSGGCC GCCAAATMAA TAACCGTKTT      240
AACKCAGGCN ACGGCCAACG GGYCCCGCCC AACCAAGCNA CCTCCCCSCC NATAGGYCCG      300
GTGGGGGCTG CCKTATYKCC AASTCGTCAY CTCNACGGGM CGGYCCMCWT TCCGCCTCAT      360
CCGTCTCTCC TTMMATTTTC CRTCCACYKG GCGGGGAACY TTTTNYCNC CTTTGSCMAN      420
CACCNAAGGY CNAAAATTNC CCMTGCKKYG SNNCAAAYGR GATTGGGGTY CGKKTNTNT      480
TCNMCCMAAC CCCNNTTTNA CGCCCCMATC CCYTWATACC CCCWWMCMNS ANGKTTGNSA      540
AAKTNNCCCC AAATRCAAA MTTCTTCGCC NTTMTWMCY YYCCTTTCCC CMCCWNAAA      600
GGSCCRCCYY TCGGGAANTY TCCCNCAAA AWTCAWCCM TTTCCCNCCA AGAAWTTCSG      660

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SACTCCTTTN	TTCNGGGNAM	ATANATYYTT	YCKTNGGGGSK	TTCCGMTCNC	AMMAATNTCC	720
RGGGKAAMCC	AGKNTNNTCC	YYYYCCCCAA	NNTYCCYKGG	RMCYNNYYCY	TTAAANRASR	780
SAACCKSGG	GKCYNCNCSS	TARCCCCCAM	KAAAAATTTCC	CCSSKTTTC	TYNNKKMRW	840
GCCCCSAAM	ACTMTWAYTT	TCCCKCGMNN	TTTSYCKCS	KCAMWMMTG	KKNCTTTTTT	900
YCSCMATAMA	CTTNGGKCCT	NTCNYGSGCG	CMAAANAAGG	CGCGSTTCTN	TTCWMAMACA	960
YNTSGNMMMA	SAAKAKWATA	AWNNTTRKKYK	TKNNCCCNCC	CKCKCTTSNN	TNKCCMCSKS	1020
GGGKNWNKKR	GWCTCCWCNC	CKCCCNCKNK	CKKWATMCCC	CCCCSKCCGM	NCMMNTTTKT	1080
CCC						1083

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GGGGNNKYAT	MCAYCWTCTS	YACSGGGMNC	TATTGCGGCC	GCAWYTINGTM	GASAGATCTC	60
GAAYTCGGCA	MGAAAAAAGW	GATGTGCTGG	ACCTTMCCGC	GCGGGACGCR	ACCRACAAAG	120
RAASCGCGCC	ANAATATTGG	CCACAKTTGG	TCACATATTT	ACCCAATTMT	AYCAGGGAYT	180
MCCATTCKKG	GGACCRACCG	CACAATCCCR	ATSKTGGTTT	GCRAACCCTR	ACCGTCCCCA	240
MYTYCGCCRA	STTGAACCG	GGCRAAAAAA	CGGCCRAAWY	CTCGCCCTGA	NTCCCGCTCS	300
GCGCNAATAA	CTAGGCCCCAT	TKAACGGAAC	CGGNGGCCSC	NANTTGGCCA	ACAGGTCCTR	360
ACAAAGGGGC	CCGASYCGG	CCGWTCCTCW	TTYCACNCCC	TNKTCTCKTG	CCGAATYCGG	420
WTCCRATNYC	CCWTGGGCCT	TKTCKYCKYC	KYCGGTNCCA	AWTCTNGGTA	TNCTATRGKG	480
TCCCCTAAAT	SCANATCTGG	GCKYCCATTT	NCTGGSNTTC	NATTTAMMAN	SRRCGGTTCT	540
TTCWTTCCRA	AACCGSNTGG	GCCCNMCCA	AAAAATGATN	ATAATAATGK	YGSCTTTCAA	600
ACCCCGCCCC	CCCATTCTRW	CSGTTCCANC	CCCCNGNGGT	TAAGKTGGGA	ATTTYTNAMC	660
YCNARGCCCT	NATTTSGGNA	AAAACCYC	GGGYCTCAA	CMNYTTTTTT	GSKSSNTCGG	720
GCTCRTTSC	CAAAACCCAA	ATTNTYNYGG	GGYCKTNAA	ACMCGGYCRC	RCCGGAAATT	780
TTTTTGTTTC	AACCCCAACC	TTTTCAASCC	NTTTTTYTYT	TRCCSSCSMN	TNGSSGGGNT	840
KSSCNTTCY	RARKKCCNMN	GGGGGWYCYN	CCCCRMNTTT	CTTTTTTTTT	CCGTNNMAAM	900
NGKTTCTTCA	AASMCCCCC	SCCCCNNSAA	ACCCCTNAR	GTTTTYCMMA	AANNWYNNGN	960
KNCCCCCCCC	MMNAAAAAY	YSCCCGNRN	ACSMNNGGGA	MCCCCGGSN	NTTRKTTTTT	1020
TNCMSGYCCC	CSRMASYTT	TKAMAMANRR	GAMNSMTTTY	TNNRGNWNK		1069

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

NGNGGGGKWK	MATACATCWT	TCTTCACGSG	GGATCWATTG	CGGGCCGCAW	TCTNGTMCAA	60
SAGATCTCGA	TYTCGGGCAM	NACCCACCWC	TCCRAAAAAA	ACCRAAWCT	CGGGSKCTYC	120
GARAAGTGTT	CCCCGCKTTR	AATTTAACAA	ATTCAAGTGC	ANAGTGTCAC	GGCKTTACWT	180

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YCCCGGCAAA	GGGGCCACAA	CCTGCAGRGA	SCACYCRATG	GKTGYTGKTS	CNCGGGCGGG	240
CCGKTNAA	GGACCTGCCT	GGGKTGCSC	TMCAANATC	WYCCGCGGGT	YCGCTGGRAT	300
MCNCAGGGT	GTCAAAAAAC	CGCAAACAGG	CACSCCANCC	NTTTACGGGS	CTTAAAANGA	360
AAAAGGGCTG	ATGCCCCCAA	GGGGGCCCCG	NCCCAACCTT	CCGTTGGTCA	ACAACCCGGT	420
CTCTCKTGCC	RAATCCGRWT	CCRATNYCNC	CWTGGCCTTK	TCKYCTYCTY	CGGTACCCAA	480
ATCTGGGTAT	CCTATASTGT	CCCCTAAWTT	CCAAATCTGG	GCTGTCCAAT	TSCTTGGCNT	540
TCCAAATTTA	CCANCAACGG	TTTCTTNCAT	NCCAAAAACC	GNTKGGCKCC	NRACCCRAAA	600
AAATGAATAA	TAATAANNGG	KCNNTTYCNA	ACCNCCCCCC	CCCNATTCCA	TYSNGTTCCA	660
NMNCCCCCAG	NGGKTAGGTK	GGGAAANYYC	TCMACCYCA	ANCCCTWARS	TTTTNGRAAT	720
KAAACCCTYC	YCNNGGTCWW	TYMAAAAAAMA	NTTATTTGGN	NGNTTTCGGG	MWNCKRKNST	780
SCCAAAATCC	MAAATANTTT	YYTGGTYCNA	TWAAAAAMCG	YGNCCMNCCC	GGAAAAWTTT	840
TTNTGKT TSA	ACCCCAAAAC	YTTTTCMNAA	NCSSKTTTTY	CYTTCCCCCC	AMNWTGGGYS	900
GGGNATKGYG	SCYTNTCTTA	TKTKYTYMTW	CMGGGGGGNN	MKMTCCMMCCC	CCMTTTYCY	960
NYWRTTTTTN	KCCCCKTNMR	NNRAANNGGN	YTCSYNANAA	AAGCNCCCCC	SCCKNCCCNA	1020
AAAAWCCCN	NNNARAKTNT	TTMKANNRMN	SKCNKNGKY	YCCCCCCCWC	YNMNNAAAAA	1080
AATMYCCNCC	RASANMCASM	NMGGRGNRSC	CCCCCCCSTT	NNNNTMTTNT	TTTTTTC SRA	1140
GAGCKCCSCG	MNNANMKNCK	CTTTTTCNC	NNGNNGNNGN	GGNGMNCKCC	CCNAGAAMWK	1200
CTKSTCCCKS						1210

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

NGSSSNGNNA	TMCATCWYCT	GYACSGGGMT	CWATTGCGGC	CGCAACTNGT	MAASAGATCT	60
CGAAYTCGGC	AAKANACACC	ACCGCCGTGT	MTATACACCG	CAAAATGTTCT	GTKTGCCAAA	120
ACCGAGACGC	GCCGGCCGCG	GGGYTCCAAC	GCKTTACYTR	ACCCGCCAGY	TCAGTGTTRA	180
AACCGGTGYT	RAGGGCCGCA	CCCAACWTAA	ACGCTTTAKC	CAAGRAWYTG	GKTGGCCCCG	240
AGCCACCTGY	TGTGGYTGCC	CTCWYCGGTG	GTAGCGCCGG	TTANCGCCGG	TTGCGCGYTC	300
AMCASCSCGC	CGGTRATCCC	AKCNWTCCCC	CGGCCMRACC	CACCGGGCAC	TTTGRACGGT	360
GCCGCCAATT	CAAAYCKYCT	GRWTCCTTCM	AAACACCACR	AAGGCCACCM	CCMSCACCNA	420
ATMGGGRACT	TTAAGGCCCA	GGCAAAACCT	NTRAKNCCT	CCCGGGCRAA	GGTCCSGCAA	480
SCRATCCMAA	AAAACCKNAT	TTCCCCCAGC	AKCAACCCAA	MMCGSTTTGC	TGCTTCCGGA	540
TTCGAAMCCA	ATTMCWGGKT	NCNWGGGAAA	AACASCNNCC	NWTAKCCMGG	CCCMCGGGCA	600
ATTTCSGRAA	SAACCCCTNY	CCCGGGTTTT	YCCTGCTCMG	GCCCAANACC	CCCGGGAATC	660
AAAAASGGTC	GGNCAAANGG	GCMAAACCCS	SACCCMACTT	WTTCCRCCTN	GGGGGGSCWN	720
CKNGTTTTAA	AWKSCCTCY	CTSCCCAAAY	TCGGKCMAAA	NNGRKTGGK	TTNGGCNACC	780
NTTTCGGK	CCGGGKGGK	WGKYCTMNMA	CSTTTNTTTT	SCCCYKAAA	NYSCCCCCCC	840
CGGSSCCCCG	CCCGGGGGGA	NNTTTT TAMA	GKKTYYCCCT	CCCCAMAAAA	ANACCCNYC	900
CCSGGSCCCT	TTKRWAAAMN	KCTSCCCNG	GNNGGGGKCM	GGKTTATTMT	NNNCCSCCCC	960
TCCGCGSAAA	AAATAKMTTT	SYCCCCCNC	CTCKKNCKNR	GKAMSMSCGC	TCCCYCTCNC	1020
GCNKNTWAAN	ARSNCCKKNN	CCNCYKCCGS	NSNGKCNWCD	NCCSTSSNCT	NKGCNCKNCN	1080
KAAANAAYNC	NGSMSTSSMN	CNKCC				1105

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

NGSNSNKNNN	TAMAYCWYYC	TSCACSNNGA	ACWANTGCGG	CCRMAWCTNS	TMKASAGATC	60
TMGAAYTCGG	CAAGAGCGGC	AAGAGTGTGT	GCATCTGGTC	ANAGTSTMMA	CRCGGTGCCG	120
CSGGTGKGTR	GASCACMCAT	NTGCGRACAC	CAAACCKTC	GCGGGYCACC	GGCKTCGCCT	180
GCAAAWYCCT	CCAGGCCACC	TCRAACAAYW	YCTYCTGCAA	CGCARGCCGT	TYCGCGGCCG	240
RATCCTGGKT	CASYCGCCK	TGCGGTGCCC	AAGKTACTGG	CSCAYCAAAA	CCGCTCCGGG	300
RAACRAACKT	AAWYTGCCG	AATTTCNTTC	CCCTGCGCCT	TGATAAATTT	NTNAAGCCAC	360
CGCAAMCCTY	CGGGCKTCTC	CTCKTGCCRA	ATYCGRWTCC	RATAYCGCCA	TGGCCTNKTC	420
KXCTYCKYCS	GTACCCAAAT	CTTGGGTATC	CTATANTKTC	CCWAAANRCA	AWTCTGGGCK	480
KTCCATKTSC	TGGSKTCCRA	ATTTAMMACA	NCGGTTTCTT	TCWTACCAAA	AACCSNTGGG	540
CCCCRACCRA	AAAAGATAA	TAATAAKGTG	CWWWCAAAAC	CCCGCCCCCC	RRTTCAAYCG	600
GTCCARCACC	CCANGNGGTN	AGGTNGGAAT	TYTMAACCCC	CAGCCCATAA	SNTTNSGNAA	660
AAACCCCCCN	GGGYMYCAAA	AMMCTTTTTG	GGGMTTCSGS	CCATKGYKCC	AAAACCAAAA	720
TMTTTCYGGT	CRWAAAAACC	GGCCCNCCCG	NAAATTTTTT	GKCAACCCCA	AACCTTTMAM	780
CCNNNTTCYY	YCCNSACAA	TNGSGGNKN	NGSSCNTTYT	TWTTYYNNA	GGGGGRRWC	840
SNCCCCNAAN	YCCNAANKG	NKCCCGSNMA	AAAGAGANTT	YCMKAAAAAC	CCCCNCNCCC	900
NAAAYACCCC	MAAAKWTTTCM	AAASMSCNNG	YCCCCC			936

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1042 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NNNGNKNNNY	ATMMAYTCWY	YCTSCACCSG	GGNNWCWATT	GCGGCCRMAW	KCTTGTMMAAS	60
AGATCTMNA	YTCGGCACAG	ASSSGCACAG	ASCCGCGGCG	CTATYCMYCC	GYTGCTCATG	120
CTCAACACGC	TCKTCGGCGW	GRATAATGGC	NCGCCGCCGG	CGCCAACACG	YTCAAYTGCT	180
TCGCCAACGC	CATATNTCAA	CAAGGTRATA	AAASCAAAAC	CGCSCGCCGY	GCCCTTGGGC	240
SCGGRAASCG	GTGCCAACCC	RAAACNCKTT	GGGCACYCGG	KTSRACTTTA	AASGGTAATC	300
TCKTCCTCCT	GGGCTATGGT	GCGCCACAAA	CCTSYTGCGG	WGGGTCTGGC	CCTGGGYCAC	360
CGYCRCNTTT	TATNTNTCKK	YCTACACNCT	TKGGTYCAAC	CAACCCACTT	CACMAAATTG	420
TTTTGGGKTG	GGGSSGCCGG	YTGTNNCCGK	TAATAATCSG	NTGKTCSGCC	MYCACCGGWA	480
CCATANCCTG	GCCGGCSCTG	GCAAATTTCC	SAAATCATYT	CCTTCTGRAC	CCCCACAMRC	540
CTNSAAATCC	GRATCAATNC	CCCNKGGCTT	NTCYCTCTCN	GTRCCCAATY	TGGTTTCTAT	600
RKTNCCCYAA	TSCAATTGGS	TTYCCRTTSC	YGSTTCCAAN	TTNACAAMAS	GGTTTTTCMT	660
ACCAAAACCC	NTGGSCCNNA	CMNAAAANKA	RAAAANAKGG	KCTTTYAAAC	CCCCCCTAT	720
TCAWYCGGTN	CMRNWCCCCG	NGKAAGGKGN	GAAAYTTTHA	CCCAANCCMT	ARSTTSGNAK	780
AAACCCYYCG	GGGTSMCAAA	MKNTWTTSSC	CTTCGGMCTT	YCCAAATMSA	AAATYYTCKK	840
KRMNAAAAMC	YGNCCCCSAA	ANATTTTTGT	NAAMCCCKMA	YYTRTTWMCC	WTTTTCCYCC	900
CCMCNNSNSG	GNTNCCCTTY	TYATTTCYMM	MCRNNSGACN	CCCCMNTYTT	TWTTCKWCN	960
MMARGSNNTY	RGRMMNMNCC	CCNCCCCNAK	MTCCNCAAAK	NTTTNAACNN	NNKYCKCCCC	1020
CCCMWMNKNC	CCCMNMCMTT	TM				1042

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

NNSGSGMKKK	ATAMATCWCT	CTSYACCSNG	GMTCWATTGC	GGCCGMAWTC	TNGTMAASAG	60
ATCTCGAAYT	CGGCAAANAK	ACGCMAYGTC	AAGTGTRAYY	CGGTACACATA	TCMTCGCGNG	120
TCAAGMCCAA	AGCGGNGTCA	CCGYCTCCCT	GGGGCGCCAC	CCCCATCGGT	RATGCAACYT	180
CGCGCGCCAC	CGYCAAAAGG	KTCWTTRAGG	CGCTAAAGGT	CAMCAATTCC	TRAGGTYMCN	240
CACCGTTNTT	TGGCCCCGCC	RAWTYCTRAC	CCGCAATWTC	GGTAATCGGR	AATTTGGGCW	300
YCGGCTTGGG	CAATAAGKTN	TTGGGCAACG	GCGGRWTCYC	NCTGGCCGRA	ATTCCNCAT	360
TCCKTTAACG	GKTGRACCGT	TTYCCCGGYT	GCCGTAAYTG	YTYCNTGGGC	GCCYTCGGCC	420
CRNAGCASY	CRCTAACGGY	CMCCAGGCAA	TACCKTTGGC	TTTRAACCAC	CGGRATNAAY	480
TGKTACCCAC	YTCAASSGTS	CTGRANTTRK	TNTCNTGRAA	AANMCCACCN	AACCCGGNTT	540
RATCTGCTTC	MTCANCWTTT	SCCGGGTTCT	GCCGTTTTGR	AAYCTTNATC	CMTYCAAAAG	600
GTTTAMTTTC	CCAANRAATT	CGGYTTGCCA	CCTTGGCCGS	GGCTGGTTTM	CGMWCCCTRR	660
AMATCCNCCS	GCGGGSAAAN	AMTTSGGNTT	SGSCCGGTCC	CCCGNAATAT	YCNTGGNCCT	720
GNAAATTGSS	GGGATCCCN	GSGNAYCCGG	CCWTKGGGK	TNCCCAGTTG	GWACAATTYC	780
WKCCGTTCCA	AACCCGGGNC	CGGGGGGTGG	GSCCNTTTT	CCTMYNNAAA	AAGKGTTTGN	840
NYTTTTTCCG	CNRAANTTCA	CCSKCNKTNT	GGNCCNAACY	YYYCAANTTC	CANACCTTTA	900
AASAAANCYK	YGKTYCCCC	TTTTMCCSGS	SANCCCCCM	NMSSKNCGGG	AAAAAAAGNK	960
TYNGCCTTAN	CNSNKTKT	TNKTYCCCC	NMWNNSNMCY	NCBKCKNKRY	NGNSNMNCCT	1020
MKYSKCN	NNNNKCGN	GSNCSGMKYM	CMNNCNGMYK	NGNKSNNCCC	MSC	1073

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GNSNGNKNTN	TMCAICYWYCT	SCACSGGGTC	TATTGCGGCC	GCAATYTNGT	CKASAGATCT	60
CGATYTCGGC	AMNANAARTG	TCGTGCTCAA	TTTCAGKKTG	GTCKTCAAAY	GGGCCAGGCC	120
GNGACCRACA	CCCTGNGTCA	CCCAAAANAC	CAACAGCWTC	AAATWTC AAG	GCCRAGGCSC	180
TRTCAATYCC	CRASCAKTTA	ACCGTKTCCW	TCRAAGGTGC	CRAACCAGGC	ACCCAGYTCA	240
CCGCCSGGCA	AWTCGCGCTG	CCGGCCGGTN	TCAGCCTGAT	TYCTGACCCT	RWTCTGTS GG	300
TGGYCAMCNT	GGTGAAGGCC	CWWCCGCCNA	AGAACTGGAG	GGCRAATTCC	CAGGANCCNA	360
GRAACCCNAG	GAACCCGCGG	TAKAANCCGG	CRAAACCRAG	GCCGYTGGCN	ATTCCNATTA	420
NAMSGGTTTG	CRACNTGGCC	RAACCGTTTTY	CTTGGTCGGC	CTCGGCAACC	CTGGACCANT	480
TACCCCKTNC	CCGGNMCMAC	CYCGGGTNCT	TGKYCCCAAT	NTGCTCCCCG	GNRANTNGGC	540
CNAATTCCAG	GGCNCCANCT	TTCCGGCCCN	AATTCCCYTG	GTTAATCACC	GGGCNCNCCT	600
GGTTTGGGC	AACCCNCYS	CTTMTTTAAA	CATTCCGSCC	CAAATGGGNC	STTGSAAAT	660

TCTNTYCGGT	GGGGCSGGCR	ANMYTTCTCT	YCCNAASAN	CTTAMYCCAN	TTCGSSNTCC	720
CGGKCAAAWS	NGGGGGGGNA	AAGGGCCCCC	CGGNTSCKCC	GGGGKKGCCC	CYGGKTTCAA	780
AANTTTCSGG	GKTSTMSCGG	NVTCSCCCCC	CSGCCAAGRA	CCGNGGTTTT	TTTTTGAACC	840
KCMANTCSSA	AMCCGCCSSC	CCMAAAGGS	GCCTNAAWGR	RAYTTNKSCC	CNNAAACSGG	900
CCCCAKYTY	SGGKTTCNNC	CNCCSGKKGT	CCMTSTTTMM	MRCCCTTGN	GNKTTTTAN	960
MGSCCTTNC	CACCCCYCK	GGGKCSMNNA	GAAKTMYWKC	CNGGGGNAN	RSCCCCCNN	1020
GSKGGGGKG	MGAGYSCCKT	CTKGCNCNN	YKNTTCCCC	C		1061

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GNNGNNNKWN	ATMCAYCWYY	CTSCACCSGG	GMTCWATTGC	GGCCGCAWKY	TNGTMAASAG	60
ATCTMGAAYT	CGGCACANAG	CGGCACAGAG	TGTGTGCATC	TGTGTCANAG	CTGTCAACGC	120
GGTGCCGCSG	GTGGTRASCA	CMCATTGCGR	AACACCAAAC	CCGTCCGCGG	GYCACC GGCK	180
TCGCCTGCAA	AAYCCTCCAG	GCCACCYCRA	AACAAYWYCT	CCTGCAACSC	ARSCCGTTYC	240
GCGGCCGRAT	CCTGGKYCAS	YTCGCKTGC	GGTGCGCCAA	GGTACTGGCS	CWYCRANACC	300
GCTYCGGGRA	ACCNAACGTA	AATCTTGCCN	AATTTGCNTT	CCCCCTSCCC	TTRATNAATT	360
TGTTAAACCA	CGCAAACCTY	CGGGCKTCTC	CTCKTGCCRA	WTCCGRWTCC	RATNYCGCCA	420
TGGCCTNKTC	KYCTYCKYCS	GTMCCCCAAT	CTTGGTATCC	TATATTGTCC	CTAAATGCAA	480
ATCTKGGCTG	TCCATNTGCT	GGCGTTCAAA	TTWAMANAG	NGGTTTCTTY	CTTCCNAAAC	540
CCSTTGCCCC	CAAACCNAAA	AATGATNATA	ATAATGGTGC	TNTCAAACCC	CGCNCCCATY	600
CNATCSGKCC	AMMCCCCRGN	GGKTANKKGG	GNAATTCTMM	AACCCCAAGC	CATAASNTTG	660
SGANAAACCY	NCNCMGGYCA	CCAAAACANY	NTTNTTGGNY	SSNTTCGGMN	YCATGGCTNN	720
CMAAAACCCA	AATACTNYYG	GGYCCAATAA	AAMMSGGYC	SAMCCGAAA	WTTTTYTTGN	780
KYNAAACCNA	AAKCTTTTTT	CNAACCCDAN	WNTYCCTNCC	RCRCMANTGG	CNSGGARTKT	840
SSSCTTNCCA	ATGKYCCMAA	AGNGGGRANA	CCARCCCCAA	TTCTTNNNTN	KNKNCCCNST	900
TRNAAAAGGG	GKNTYNCMAA	AASCNCCNCC	NCNCTCCCAA	AAKAMCCCN	AAAGAKNTCN	960
NAANASKYSN	NNNSCCCCC	CCMMMN				986

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

NGNGGGNKRN	ATMMAYCWCT	SATYYACCSN	GGMNMWATTG	CGGCCRMWAT	CTNGTMKASA	60
GATCTMGAAG	YTCGGCAAAG	AGYATKCTCG	GGGGCCAGAT	TTNTGGCCCC	CAACCGCCGC	120
ACTTTGCAYW	TCAACAKTCC	SGGTGCCCCA	AAAAAWTCWT	ACCCCATMC	TYCKTGASM	180
ASYTGCGCCC	RATTRAACAC	CCGGCCGGCW	TGCTGCGCCA	GGTATTYCAS	CAGYTCAAAY	240
YCTTTKTAGK	TAAAATCCAG	CSGGCGGCCA	CNCAGCCGGG	CGGKTAGGT	GCCTYCRTCA	300

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ATMACCAGCY	CGCCCAGGGY	CACCTTGCCC	AAAAYCTCCT	GGGTCAGCCA	AATTYCCGCS	360
CCGGCCAACM	ACCANCCGCA	TYCTGGCNTC	AATCYCACCG	GGCCCGGTGY	TAAAMMANMA	420
GRATCTCKTC	MANCCCCCAN	TCAGCSYTNA	CNGCMACAGC	CCGCCTTCTT	CAMACCGCCA	480
RTACCGGGWT	CAACCGGCCS	GTCAAACCTCA	ACAGGCGGNC	AGGCCTCCCC	CGGANSAAAG	540
GTCTTACSCC	NNYAANAAAA	MAAGNTCTGT	TTTCCCCCTC	CASAASNAAA	AANCCCCSGC	600
CGGGCCTTCN	NMMGGGTTTG	GGGMANANAA	AARCNC CGGN	GGAACGNATC	CGAAAMCTCC	660
CAAGTCNCMT	TWAWAACYCN	NNAACCCCCC	ANTTTTGGGA	AAGGNTCCCC	NTTMYCCCCC	720
TTTTASGKTS	GGGMMYYCTY	TAAAAAAAT	CCCCAAAAAG	CCCCGGGAAG	GGTCMAMCTG	780
GGNAAATTTT	CAAMCCNWK	TTNTTYNGGT	TMCGGGGGRA	AATTYCNCCTC	CCYNNNNGGG	840
CSSGSNNNAT	TAYGGMSNMT	TTTNNAAWTM	NSGKKTSAAM	YNNKCCMNNN	SNNMSMANNK	900
TNAMCKCCCN	CCTCNGNGKY	CSCYNCCCCS	GNAGNGGRAS	MKCCNANMAA	AYASGNTTNK	960
CGGAAMMCNN	AATKGNNNSC	CCGGASMCMN	NNNMAAATMT	CNCNKCNSEN	AANRGMRAACN	1020
CCCNSNSGMN	RRGAARMTNY	YCCCCCGSKM	GKGNKAAAAG	GKYCCCCCCM	AAAG	1074

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

NGNGNCNKNT	MTACATCWTT	CTGCACCSGG	GNTCWANTGC	GGCCGCAWKY	TTGTGASAG	60
ATCTCGAAYT	CGGCAMGAGG	ACWCTCGCRA	CGCCCCACA	NACTCTGGCG	TGTGTACCCC	120
ATTGNGCGCK	TCACGCGCCC	AYTGANCCAK	TNCACTGGGG	TGCCGTYCGC	CKTGCGCGGC	180
GGCCTCACGG	CKCTSCWTCT	RAAGGCWTGG	CGCACCGCAT	TCGGTTTTCT	RAACGCTGGG	240
AAAWTGGCCA	GCCGTCTGGC	TCATGGGNTC	TACGCAACGC	CNGCCCCAA	CRCTTTCTTA	300
AATCCGGYCC	NTCCTGANCS	CTTTGAAYCC	CGGGGSAAGA	ACTGGTTGCS	CNCGAYCTGC	360
TCGAACCTTRK	TCNAAATCCC	GCANAKTGTT	TCNTAMGYCC	CNCCGGAAGG	NGAACCTACT	420
TTCNGGWANG	TCGGCNKCCG	GCGCTTATCA	STCCTGATCA	ACGGGGAACT	GGYKNNSTTG	480
KGGGAAAAAG	RRCTCAATG	MTYGGTCKKC	GCTGCGKANC	CGSCCCTGK	GYCGCNAATG	540
GAAGGCSMAG	GGTTAANGCC	MTTYCNYCCR	RSCCGTSTGA	SGKWTTYCGG	MGGANKAMNN	600
NNKMAMWTTK	TCRNGGGCCW	ATSTSCCGGG	CKSTTAKAGA	ANACTYCKKW	WCCGTNTYSC	660
SAAAGNTKCS	GCGMGTTTTS	SCCKMGANGN	YCTGATTTSA	GGGGGKYKCC	CCCCGGGTYC	720
CGAAWKWKY	CCYAGGGGGM	GNYSAGCSC	CGMNNATNAG	AGNAAGGKTT	RYGSTSKNCC	780
TYTNKGAC	WSCNNCWSAK	ANAACNNKKT	TGCSCCNTMS	AGNKTNGKRT	YCCNKTSTTC	840
TAAGAGGAGC	TATKMKCGCC	CKTGGANGMM	GAGWGMGCGC	KYCCCSNKRT	TCNTNGWAAA	900
TATKSAGMGG	TKCCGMAGMK	CCSCGTTTCT	TKTGANAAMN	MSMRKNKKTG	CGMGYTCTSC	960
GGGNTTTGTA	GAGTAKTCGS	CSCSSMWGAC	WCSGMCMGNG	AGKNKTNNNTS	YANTGARCXY	1020
MNNSKTMKMT	MSCSCGCGNA	GGAGNGCCCC	CSANGMSTGY	NKGGNMSSNG	ARAKGATGGS	1080
GGCCNCGMNN	MGMGGANMGA	SANNGMGGMR	GGGGGKTGKC	TCKCSCCGNS	CSANGRAGAA	1140
GKTCNGSCGC	CGMGGKYGKT	KTKTKNKTGG	YSTCMSSMMM	NAGAAAAGAG	AGGGC	1195

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

CCATCTGATC	GTTGGCAACC	AGCATCGCAG	TGGGAACGAT	GCCCTCATTC	AGCATTGCA	60
TGGTTTGTG	AAAACCGGAC	ATGGCACTCC	AGTCGCCTTC	CCGTTCCGCT	ATCGGCTGAA	120
TTTGATTGCG	AGTGAGATAT	TTATGCCAGC	CAGCCAGACG	CAGACGCGCC	GAGACAGAAC	180
TTAATGGGCC	CGCTAACAGC	GCGATTTGCT	GGTGACCCAA	TGCGACCAGA	TGCTCCACGC	240
CCAGTCGCGT	ACCGTCTTCA	TGGGAGAAAA	TAATACTGTT	GATGGGTGTC	TGGTCAGAGA	300
CATCAAGAAA	TAACGCCGGA	ACATTAGTGC	AGGCAGCTTC	CACAGCAATG	GCATCCTGGT	360
CATCCAGCGG	ATAGTTAATG	ATCAGCCCAC	TGACGCGTTG	CGCGAGAAGA	TTGTGCACCG	420
CCGCTTTACA	GGCTTCGACG	CCGCTTCGTT	CTACCATCGA	CACCACCACG	CTGGCACCCA	480
GTTGATCGGC	GCGAGATTTA	ATCGCCGCGA	CAATTTGCGA	CGGCGCGTGC	AGGGCCAGAC	540
TGGAGGTGGC	AACGCCAATC	AGCAACGACT	GTTTGCCCGC	CAGTTGTTGT	GCCACGCGGT	600
TGGGAATGTA	ATTGAGCTCC	GCCATCGCCG	CTTCCACTTT	TTCCCGCGTT	TTGCGAGAAA	660
CGTGCGTGGC	CTGCTTCACC	ACGCGGGGAA	CGGTCTGATA	AGAGACACCG	GCATACTCTG	720
CGACATCGTA	TAACGTTACT	GGTTTCACAT	TCACCACCTT	GAATTGACTC	TCTTCCGGGC	780
GCTATCATGC	CATACCGCGA	AAGGTTTTGC	GCCATTCGAT	GGTGTCCGGG	ATCTCGACGC	840
TCTCCCTTAT	GCGACTCCTG	CATTAGGAAG	CAGCCCAGTA	GTAGGTTGAG	GCCGTTGAGC	900
ACCGCCGCGG	CAAGGAATGG	TGCATGCAAG	GAGATGGCGC	CCAACAGTCC	CCCGGCCACG	960
GGGCCTGCCA	CCATACCCAC	GCCGAAACAA	GCGCTCATGA	GCCCGAAGTG	GCGAGCCCGA	1020
TCTTCCCCAT	CGGTGATGTC	GGCGATATAG	GCGCCAGCAA	CCGCACCTGT	GCGCCCGGTG	1080
ATGCCGGCCA	CGATGCGTCC	GGCGTAGAGG	ATCGAGATCT	CGATCCCGCG	AAATTAATAC	1140
GACTCACTAT	AGGGGAATTG	TGAGCGGATA	ACAATTTCCC	TCTAGAAATA	ATTTTGTTTA	1200
ACTTTAAGAA	GGAGATATAC	ATATGGGCCA	TCATCATCAT	CATCACGTGA	TCGACATCAT	1260
CGGGACACAG	CCCACATCCT	GGGAACAGGC	GGCGGCGGAG	GCGGTCCAGC	GGGCGCGGGA	1320
TAGCGTCGAT	GACATCCGCG	TCGCTCGGGT	CATTGAGCAG	GACATGGCCG	TGGACAGCGC	1380
CGGCAAGATC	ACCTACCGCA	TCAAGCTCGA	AGTGTCGTTT	AAGATGAGGC	CGGCGCAACC	1440
GAGGGGCTCG	AAACCACCGA	GCGGTTTCGC	TGAAACGGGC	GCCGGCGCCG	GTACTGTGCG	1500
GACTACCCCC	GCGTCGTCGC	CGGTGACGTT	GGCGGAGACC	GGTAGCACGC	TGCTCTACCC	1560
GCTGTTCAAC	CTGTGGGGTC	CGGCCTTTCA	CGAGAGGTAT	CCGAACGTCA	CGATCACCGC	1620
TCAGGGCACC	GGTTCTGGTG	CCGGGATCGC	GCAGGCCGCC	GCCGGGACGG	TCAACATTGG	1680
GGCCTCCGAC	GCCTATCTGT	CGGAAGGTGA	TATGGCCGCG	CACAAGGGGC	TGATGAACAT	1740
CGCGCTAGCC	ATCTCCGCTC	AGCAGGTCAA	CTACAACCTG	CCCGGAGTGA	GCGAGCACCT	1800
CAAGCTGAAC	GGAAAAGTCC	TGGCGGCCAT	GTACCAGGGC	ACCATCAAAA	CCTGGGACGA	1860
CCCGCAGATC	GCTGCGCTCA	ACCCCGGCGT	GAACCTGCCC	GGCACCGCGG	TAGTTCGCGT	1920
GCACCGCTCC	GACGGGTCCG	GTGACACCTT	CTTGTTTACC	CAGTACCTGT	CCAAGCAAGA	1980
TCCCGAGGGC	TGGGGCAAGT	CGCCCGGCTT	CGGCACCACC	GTCGACTTCC	CGGCGGTGCC	2040
GGGTGCGCTG	GGTGAGAACG	GCAACGGCGG	CATGGTGACC	GGTTGCGCCG	AGACACCGGG	2100
CTGCGTGGCC	TATATCGGCA	TCAGCTTCCT	CGACCAGGCC	AGTCAACGGG	GACTCGGCGA	2160
GGCCCAACTA	GGCAATAGCT	CTGGCAATTT	CTTGTTGCCC	GACGCGCAAA	GCATTCAGGC	2220
CGCGGCGGCT	GGCTTCGCAT	CGAAAACCCC	GGCGAACCAG	GCGATTTCTG	TGATCGACCG	2280
GCCCGCCCCG	GACGGCTACC	CGATCATCAA	CTACGAGTAC	GCCATCGTCA	ACAACCGGCA	2340
AAAGGACGCC	GCCACCGCGC	AGACCTTGCA	GGCATTCTTG	CACTGGGCGA	TCACCGACGG	2400
CAACAAGGCC	TCGTTCCCTC	ACCAGGTTCA	TTTCCAGCCG	CTGCCGCCCG	CGGTGGTGAA	2460
GTTGTCTGAC	GCGTTGATCG	CGACGATTTT	CAGCGCTGAG	ATGAAGACCG	ATGCCGCTAC	2520
CCTCGCGCAG	GAGGCAGGTA	ATTTGAGCGG	GATCTCCGGC	GACCTGAAAA	CCCAGATCGA	2580
CCAGGTGGAG	TCGACGGCAG	GTTCTGTTGA	GGGCCAGTGG	CGCGGCGCGG	CGGGGACGGC	2640
CGCCCAGGCC	GCGGTGGTGC	GCTTCCAAGA	AGCAGCCAAT	AAGCAGAAGC	AGGAACTCGA	2700
CGAGATCTCG	ACGAATATTC	GTCAGGCCGG	CGTCCAATAC	TCGAGGGCCG	ACGAGGAGCA	2760
GCAGCAGGCG	CTGTCCCTCG	AAATGGGCTT	TGGATTGAGC	TTGCGGCTGC	CTGCTGGCTG	2820
GGTGGAGTCT	GACGCCGCCC	ACTTCGACTA	CGGTTGAGCA	CTCCTCAGCA	AAACCACCGG	2880
GGACCCGCCA	TTTCCCGGAC	AGCCGCCGCC	GGTGGCCAAT	GACACCCGTA	TCGTGCTCGG	2940
CCGGCTAGAC	CAAAAGCTTT	ACGCCAGCGC	CGAAGCCACC	GACTCCAAGG	CCGCGGCCCG	3000
GTTGGGCTCG	GACATGGGTG	AGTTCTATAT	GCCCTACCCG	GGCACCCGGA	TCAACCAGGA	3060

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AACCGTCTCG CTYGACGCCA ACGGGGTGTC TGGAAGCGCG TCGTATTACG AAGTCAAGTT 3120
 CAGCGATCCG AGTAAGCCGA ACGGCCAGAT CTGGACGGGC GTAATCGGCT CGCCCGCGGC 3180
 GAACGCACCG GACGCCGGGC CCCCTCAGCG CTGGTTGTG GTATGGCTCG GGACCGCCAA 3240
 CAACCCGGTG GACAAGGGCG CGGCCAAGGC GCTGGCCGAA TCGATCCGGC CTTTGGTTCG 3300
 CCCGCCGCCG GCGCCGGCCG GGAAGTCGC TCCTACCCCG ACGACACCGA CACCGCAGCG 3360
 GACCTTACCG GCCTGAGAA TCTGCAGATA TCCATCACAC TGGCGGCCCG TCGAGCACCA 3420
 CCACCACCAC CACTGAGATC CGGCTGCTAA CAAAGCCCGA AAGGAAGCTG AGTTGGCTGC 3480
 TGCCACCGCT GAGCAATAAC TAGCATAACC CCTTGGGGCC TCTAACGGG TCTTGAGGGG 3540
 TTTTTTGCTG AAAGGAGGAA CTATATCCCG AT 3572

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Val Gln Phe Gln Ser Gly Gly Asp Asn Ser Pro Ala Val Tyr Xaa Xaa
 1 5 10 15
 Asp Gly Xaa Arg
 20

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Thr Thr Val Pro Xaa Val Thr Glu Ala Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Thr Thr Pro Ser Xaa Val Ala Phe Ala Arg

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1

5

10

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Asp Ala Gly Lys Xaa Ala Gly Xaa Asp Val Xaa Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Thr Xaa Glu Glu Xaa Gln Glu Ser Phe Asn Ser Ala Ala Pro Gly Asn
 1 5 10 15
 Xaa Lys

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CTAGTTAGTA CTCAGTCGCA GACCGTG

27

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GCAGTGACGA ATTCACTTCG ACTCC

25

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

CATATGGGCC	ATCATCATCA	TCATCACGTG	ATCGACATCA	TCGGGACCAG	CCCCACATCC	60
TGGGAACAGG	CGGCGGCGGA	GGCGGTCCAG	CGGGCGCGGG	ATAGCGTCGA	TGACATCCGC	120
GTCGCTCGGG	TCATTGAGCA	GGACATGGCC	GTGGACAGCG	CCGGCAAGAT	CACCTACCGC	180
ATCAAGCTCG	AAGTGTCGTT	CAAGATGAGG	CCGGCGCAAC	CGAGGGGCTC	GAAACCACCG	240
AGCGGTTCGC	CTGAAACGGG	CGCCGGCGCC	GGTACTGTCTG	CGACTACCCC	CGCGTCGTCG	300
CCGGTGACGT	TGGCGGAGAC	CGGTAGCACG	CTGCTCTACC	CGCTGTTCAA	CCTGTGGGGT	360
CCGGCCTTTC	ACGAGAGGTA	TCCGAACGTC	ACGATCACCG	CTCAGGGCAC	CGGTTCTGGT	420
GCCGGGATCG	CGCAGGCCGC	CGCCGGGACG	GTCAACATTG	GGGCCTCCGA	CGCCTATCTG	480
TCGGAAGGTG	ATATGGCCGC	GCACAAGGGG	CTGATGAACA	TCGCGCTAGC	CATCTCCGCT	540
CAGCAGGTCA	ACTACAACCT	GCCCGGAGTG	AGCGAGCACC	TCAAGCTGAA	CGGAAAAGTC	600
CTGGCGGCCA	TGTACCAGGG	CACCATCAAA	ACCTGGGACG	ACCCGCAGAT	CGCTGCGCTC	660
AACCCCGGCG	TGAACCTGCC	CGGCACCGCG	GTAGTTCGCG	TGCACCGCTC	CGACGGGTCC	720
GGTGACACCT	TCTTGTTTAC	CCAGTACCTG	TCCAAGCAAG	ATCCCGAGGG	CTGGGGCAAG	780
TCGCCCCGGT	TCGGCACCAC	CGTCGACTTC	CCGGCGGTGC	CGGGTGCGCT	GGGTGAGAAC	840
GGCAACGGCG	GCATGGTGAC	CGGTTGCGCC	GAGACACCGG	GCTGCGTGGC	CTATATCGGC	900
ATCAGCTTCC	TCGACCAGGC	CAGTCAACGG	GGACTCGGCG	AGGCCCAACT	AGGCAATAGC	960
TCTGGCAATT	TCTTGTTGCC	CGACGCGCAA	AGCATTCAGG	CCGCGGCGGC	TGGCTTCGCA	1020
TCGAAAACCC	CGGCGAACCA	GGCGATTTCG	ATGATCGACG	GGCCCGCCCC	GGACGGCTAC	1080
CCGATCATCA	ACTACGAGTA	CGCCATCGTC	AACAACCGGC	AAAAGGACGC	CGCCACCGCG	1140
CAGACCTTGC	AGGCATTTCT	GCACTGGGCG	ATCACCAGCG	GCAACAAGGC	CTCGTTCTCTC	1200
GACCAGGTTT	ATTTCCAGCC	GCTGCCGCC	GCGGTGGTGA	AGTTGTCTGA	CGCGTTGATC	1260
GCGACGATTT	CCAGCGCTGA	GATGAAGACC	GATGCCGCTA	CCCTCGCGCA	GGAGGCAGGT	1320
AATTTTCGAG	GGATCTCCGG	CGACCTGAAA	ACCCAGATCG	ACCAGGTGGA	GTGACGGCA	1380
GGTTCGTTGC	AGGGCCAGTG	GCGCGGCGCG	GCGGGGACGG	CCGCCAGGC	CGCGGTGGTG	1440
CGCTTCCAAG	AAGCAGCCAA	TAAGCAGAAG	CAGGAACCTG	ACGAGATCTC	GACGAATATT	1500
CGTCAGGCCG	GCGTCCAATA	CTCGAGGGCC	GACGAGGAGC	AGCAGCAGGC	GCTGTCTCTG	1560
CAAATGGGCT	TTGTGCCCAC	AACGGCCGCC	TCGCCGCCGT	CGACCGCTGC	AGCGCCACCC	1620
GCACCGGCGA	CACCTGTTGC	CCCCCACCA	CCGGCCGCCG	CCAACACGCC	GAATGCCAG	1680
CCGGGCGATC	CCAACGCAGC	ACCTCCGCCG	GCCGACCCGA	ACGCACCGCC	GCCACCTGTC	1740
ATTGCCCCAA	ACGCACCCCA	ACCTGTCCGG	ATCGACAACC	CGGTTGGAGG	ATTGAGCTTC	1800
GCGCTGCCTG	CTGGCTGGGT	GGAGTCTGAC	GCCGCCCACT	TCGACTACGG	TTCAGCACTC	1860
CTCAGCAAAA	CCACCGGGGA	CCCGCCATT	CCCGGACAGC	CGCCGCCGGT	GGCCAATGAC	1920
ACCCGTATCG	TGCTCGGCCG	GCTAGACCAA	AAGCTTTTACG	CCAGCGCCGA	AGCCACCGAC	1980
TCCAAGGCCG	CGGCCCGGTT	GGGCTCGGAC	ATGGGTGAGT	TCTATATGCC	CTACCCGGGC	2040
ACCCGGATCA	ACCAGGAAAC	CGTCTCGCTC	GACGCCAACG	GGGTGTCTGG	AAGCGCGTCG	2100
TATTACGAAG	TCAAGTTCAG	CGATCCGAGT	AAGCCGAACG	GCCAGATCTG	GACGGGCGTA	2160

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ATCGGCTCGC	CCGCGGCGAA	CGCACC GGAC	GCCGGGCCCC	CTCAGCGCTG	GTTTGTGGTA	2220
TGGCTCGGGA	CCGCCAACAA	CCCGGTGGAC	AAGGGCGCGG	CCAAGGCGCT	GGCCGAATCG	2280
ATCCGGCCTT	TGGTCGCCCC	GCCGCCGGCG	CCGGCACC GG	CTCCTGCAGA	GCCCCGTCCG	2340
GCGCCGGCGC	CGGCCGGGGA	AGTCGCTCCT	ACCCCGACGA	CACCGACACC	GCAGCGGACC	2400
TTACCGGCCT	GA					2412

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met	Gly	His	His	His	His	His	His	Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser
1				5					10					15	
Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala	Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg
			20					25					30		
Asp	Ser	Val	Asp	Asp	Ile	Arg	Val	Ala	Arg	Val	Ile	Glu	Gln	Asp	Met
		35				40					45				
Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile	Thr	Tyr	Arg	Ile	Lys	Leu	Glu	Val
	50					55					60				
Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln	Pro	Arg	Gly	Ser	Lys	Pro	Pro	Ser
65				70					75					80	
Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro
				85				90						95	
Ala	Ser	Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr
			100					105					110		
Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn
		115				120					125				
Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln
	130				135					140					
Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser
145				150					155					160	
Glu	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala
			165					170					175		
Ile	Ser	Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His
		180				185						190			
Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile
	195				200						205				
Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn
	210				215						220				
Leu	Pro	Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly
225				230					235					240	
Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly
		245						250					255		
Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val
		260					265						270		
Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys
	275				280						285				
Ala	Glu	Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp

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290		295		300
Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser				
305		310		315
Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala				320
		325		330
Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp				335
		340		345
Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile				350
		355		360
Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala				365
		370		375
Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp				380
385		390		395
Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp				400
		405		410
Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala				415
		420		425
Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu				430
		435		440
Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly				445
		450		455
Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg				460
465		470		475
Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser				480
		485		490
Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu				495
		500		505
Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala				510
		515		520
Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro				525
		530		535
Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro				540
545		550		555
Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro				560
		565		570
Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn				575
		580		585
Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser				590
		595		600
Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr				605
610		615		620
Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr				625
		630		635
Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu				640
		645		650
Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu				655
		660		665
Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser				670
		675		680
Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys				685
		690		695
Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile				700
705		710		715
Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp				720
		725		730
				735

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Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GGATCCAAAC CACCGAGCGG TTCGCCTGAA ACGG

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(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CGCTGCGAAT TCACCTCCGG AGGAAATCGT CGCGATC

37

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

CATATGGGCC ATCATCATCA TCATCACGGA TCCAAACCAC CGAGCGGTTC GCCTGAAACG	60
GGCGCCGGCG CCGGTACTGT CGCGACTACC CCCGCGTCGT CGCCGGTGAC GTTGGCGGAG	120
ACCGGTAGCA CGCTGCTCTA CCCGCTGTTT AACCTGTGGG GTCCGGCCTT TCACGAGAGG	180
TATCCGAACG TCACGATCAC CGTCTAGGGC ACCGGTTCTG GTGCCGGGAT CGCGCAGGCC	240

GCCGCCGGGA CGGTCAACAT TGGGGCCTCC GACGCCTATC TGTCGGAAGG TGATATGGCC 300
 GCGCACAAGG GGCTGATGAA CATCGCGCTA GCCATCTCCG CTCAGCAGGT CAACTACAAC 360
 CTGCCCCGAG TGAGCGAGCA CCTCAAGCTG AACGGAAAAG TCCTGGCGGC CATGTACCAG 420
 GGCACCATCA AAACCTGGGA CGACCCGCG AGTCGTGCGC TCAACCCCGG CGTGAACCTG 480
 CCCGGCACCG CGGTAGTTCC GCTGCACCGC TCCGACGGGT CCGGTGACAC CTTCTTGTTT 540
 ACCCAGTACC TGTCGAAGCA AGATCCCGAG GGCTGGGGCA AGTCGCCCGG CTTCCGGCACC 600
 ACCGTCGACT TCCCGGCGGT GCCGGGTGCG CTGGGTGAGA ACGGCAACGG CGGCATGGTG 660
 ACCGGTTGCG CCGAGACACC GGGCTGCGTG GCCTATATCG GCATCAGCTT CCTCGACCAG 720
 GCCAGTCAAC GGGGACTCGG CGAGGCCCAA CTAGGCAATA GCTCTGGCAA TTTCTTGTTG 780
 CCCGACGCGC AAAGCATTCA GGCCGCGGCG GCTGGCTTCG CATCGAAAAC CCCGGCGAAC 840
 CAGGCGATTT CGATGATCGA CGGGCCCGCC CCGGACGGCT ACCCGATCAT CAACTACGAG 900
 TACGCCATCG TCAACAACCG GCAAAAGGAC GCCGCCACCG CGCAGACCTT GCAGGCATTT 960
 CTGCACTGGG CGATCACCGA CGGCAACAAG GCCTCGTTCC TCGACCAGGT TCATTTCCAG 1020
 CCGCTGCCGC CCGCGGTGGT GAAGTTGTCT GACGCGTTGA TCGCGACGAT TTCCTCCGGA 1080
 GGTGGCAGTG GGGGAGGCTC AGGTGGAGGT TCTGGCGGGA GCGTGCCAC AACGGCCGCC 1140
 TCGCCGCCGT CGACCGCTGC AGCGCCACCC GCACCGGCGA CACCTGTTGC CCCCCACCA 1200
 CCGGCCGCCG CCAACACGCC GAATGCCAG CCGGGCGATC CCAACGCAGC ACCTCCGCCG 1260
 GCCGACCCGA ACGCACC GCCACCTGTC ATTGCCCAA ACGCACCCCA ACCTGTCCGG 1320
 ATCGACAACC CGGTTGGAGG ATTCAGCTT GCGCTGCCTG CTGGCTGGGT GGAGTCTGAC 1380
 GCCGCCCACT TCGACTACGG TTCAGCACTC CTCAGCAAAA CCACCGGGGA CCCGCCATTT 1440
 CCCGGACAGC CGCCGCCGT GGCCAATGAC ACCCGTATCG TGCTCGGCCG GCTAGACCAA 1500
 AAGCTTTACG CCAGCGCCGA AGCCACCGAC TCCAAGGCCG CGGCCCGGTT GGGCTCGGAC 1560
 ATGGGTGAGT TCTATATGCC CTACCCGGGC ACCCGGATCA ACCAGGAAAC CGTCTCGCTC 1620
 GACGCCAACG GGGTGTCTGG AAGCGCGTCG TATTACGAAG TCAAGTTCAG CGATCCGAGT 1680
 AAGCCGAACG GCCAGATCTG GACGGGCGTA ATCGGCTCGC CCGCGGCGAA CGCACCGGAC 1740
 GCCGGGCCCC CTCAGCGCTG GTTTGTGGTA TGGCTCGGGA CCGCCAACAA CCCGGTGGAC 1800
 AAGGGCGCGG CCAAGGCGCT GGCCGAATCG ATCCGGCCTT TGGTCGCCCC GCCGCCGGCG 1860
 CCGGCACCGG CTCCTGCAGA GCCCGCTCCG GCGCCGGCGC CGGCCGGGGA AGTCGCTCCT 1920
 ACCCCGACGA CACCGACACC GCAGCGGACC TTACCGGCCT GA 1962

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met Gly His His His His His His Gly Ser Lys Pro Pro Ser Gly Ser
 1 5 10 15
 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 20 25 30
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 35 40 45
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 50 55 60
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 65 70 75 80
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 85 90 95
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser

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Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	Phe	Ser	Asp	Pro	Ser	Lys
545					550					555					560
Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	Gly	Ser	Pro	Ala	Ala	Asn
				565					570						575
Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	Phe	Val	Val	Trp	Leu	Gly
			580					585						590	
Thr	Ala	Asn	Asn	Pro	Val	Asp	Lys	Gly	Ala	Ala	Lys	Ala	Leu	Ala	Glu
		595					600					605			
Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Pro	Ala	Pro	Ala	Pro	Ala	Pro
	610					615					620				
Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Gly	Glu	Val	Ala	Pro	Thr
625					630					635					640
Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu	Pro	Ala				
				645					650						

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